

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:18:06 ; Search time 270.325 Seconds  
(without alignments)  
425.847 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQVQLQQSGAEIVRPQTSV.....GSEQKLISEDLNHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395	100.0	262	4 AAB70762	Ab70762 Single ch
2	1122	80.4	264	7 ADE22920	Ade29202 Multivale
3	1002	71.8	248	2 AAW58826	Aaw58826 Human CD3
4	946.5	67.8	562	6 ABR57058	Ab70758 Plasmid p
5	942.5	67.6	594	9 ABE29087	Aeb29087 Immunokin
6	938	67.2	288	2 AAW82482	Aaw82482 Mouse bis
7	936	67.1	288	2 AAW82317	Aaw82317 Mouse bis
8	936	67.1	288	2 AAW82316	Aaw82316 Mouse OKT
9	930	66.7	539	3 AAY50823	Aay50823 Fv-antibo
10	930	66.7	554	3 AAY50822	Aay50822 Fv-antibo
11	919.5	65.9	269	8 ADR28054	Adr28054 NPB polyp
12	917.5	65.8	283	8 ADF85426	Adf85426 V122scrFv
13	911.5	65.3	267	8 ADR70320	Adr70320 Polioviru
14	909.5	65.2	267	8 ADP84954	Adp84954 Single ch
15	906	64.9	264	8 ADP84957	Adp84957 Single ch
16	905.5	64.9	263	8 ADP84958	Adp84958 Single ch
17	905.5	64.9	562	6 ABR57059	Ab70759 Plasmid p
18	905	64.9	266	8 ADP84955	Adp84955 Single ch
19	904	64.8	262	8 ADP84959	Adp84959 Polioviru
20	904	64.8	268	8 ADR70319	Adr70319 Polioviru
21	902.5	64.7	261	8 ADP84960	Adp84960 Single ch
22	902.5	64.7	265	8 ADP84956	Adp84956 Single ch
23	902	64.7	260	8 ADP84961	Adp84961 Single ch
24	901.5	64.6	259	8 ADP84962	Adp84962 Single ch

25	900	64.5	276	8 ADP84953	Adp84953 Single ch
26	900	64.5	294	9 ADZ66387	Adz66387 MOF11 ant
27	897	64.3	258	8 ADP84963	Adp84963 Single ch
28	895.5	64.2	240	6 ABJ26742	Abj26742 VEGF bind
29	895.5	64.2	240	8 ADK18245	Adk18245 Mouse VEG
30	895	64.2	268	8 ADR70385	Adr70385 Polioviru
31	895	64.2	268	8 ADR70386	Adr70386 Polioviru
32	892.5	64.0	257	8 ADP84964	Adp84964 Single ch
33	891.5	63.9	296	8 ADS20752	Ads20752 SBP tagge
34	876.5	62.8	241	2 AAW09435	Aaw09435 Anti-CD19
35	876.5	62.8	242	2 AAW09444	Aaw09444 Modified
36	875	62.7	500	9 ADV66137	Adv66137 Anti-CD3-
37	875	62.7	503	9 ADV66133	Adv66133 Anti-CD3-
38	875	62.7	503	9 ADV66135	Adv66135 Anti-CD3-
39	867.5	62.2	288	2 AAW82743	Aaw82743 Fusion pr
40	859.5	61.6	1033	9 AEB29091	Aeb29091 Immunokin
41	858	61.5	240	6 ABU07881	Abu07881 Venezuela
42	856.5	61.4	255	7 ADF72734	Adf72734 His-tagge
43	856	61.4	240	6 ABU07883	Abu07883 Venezuela
44	855	61.3	500	9 ADV66095	Adv66095 Anti-CD3-
45	855	61.3	503	9 ADV66087	Adv66087 Anti-CD3-

#### ALIGNMENTS

##### RESULT 1

AAB70762  
ID AAB70762 standard; protein; 262 AA.

XX  
AC AAB70762;

DT 18-MAY-2001 (first entry)

DE Single chain Fv antibody construct anti-CD16 VH domain protein.

XX Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;  
KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;  
KW tumor cell; natural killer cell activation; Hodgkin's disease;  
KW Reed-Sternberg disease.

XX Synthetic.

XX DE19937264-A1.

XX 15-FEB-2001.

XX 06-AUG-1999; 99DE-01037264.

XX 06-AUG-1999; 99DE-01037264.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;

XX WPI; 2001-184000/19.

XX N-PSDB; AAF61152.

XX New Fv-antibody construct, useful for treating Hodgkin and Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30 surface protein.

XX Disclosure; Page 10; 18pp; German.

XX This invention describes a novel Fv-antibody construct (I) having binding sites for a CD16 receptor and a CD30 surface protein. The invention also describes (1) expression vector encoding (I); (2) transformants containing the vector of (1); (3) preparation of (I) by culturing cells of (2); and (4) kit comprising (1) and/or the vector of (1), and CC auxiliaries such as buffers, solvents, carriers, controls and labels, or CC their replacements. The products of the invention have cytostatic activity. (I) causes lysis of CD30+, specifically tumor, cells. It CC activates natural killer cells, through the CD16 receptor, and directs CC them to CD30-expressing cells. (I) are used to treat diseases in which

CC CD30+ cells are implicated, particularly tumors and specifically Hodgkin  
 CC or Reed-Sternberg diseases. (1) have a stronger lytic action than known  
 CC bispecific antibodies, can be produced on a large scale with high purity,  
 CC and contain no components that can induce unwanted immune responses

XX Sequence 262 AA;

Query Match 100.0%; Score 1395; DB 4; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-94;  
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVQLQSGAEELVRPQTSVKISCKASGYTFNFWLGVKQRPQGHLEWIGDIYPGGYTT 60  
 DB 1 MAQVQLQSGAEELVRPQTSVKISCKASGYTFNFWLGVKQRPQGHLEWIGDIYPGGYTT 60

QY 61 NYNEKFGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVSSA 120  
 DB 61 NYNEKFGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVSSA 120

QY 121 KTPKLGSDIELTQSPKFMSTSGDRVNTYKASQNVGTNVAWFQKPGQSPKVLIIYSAS 180  
 DB 121 KTPKLGSDIELTQSPKFMSTSGDRVNTYKASQNVGTNVAWFQKPGQSPKVLIIYSAS 180

QY 181 YRYSGVDPDRFTSGSGTDFLTITISNVQSEDLAEYFCQYHTYPLTFGGGTGLEIKRADAA 240  
 DB 181 YRYSGVDPDRFTSGSGTDFLTITISNVQSEDLAEYFCQYHTYPLTFGGGTGLEIKRADAA 240

QY 241 AAGSEQKLISEEDLNSHHHHHH 262  
 DB 241 AAGSEQKLISEEDLNSHHHHHH 262

RESULT 2

AD29202  
 ID ADE29202 standard; protein; 264 AA.

AC ADE29202;

XX 29-JAN-2004 (first entry)

XX Multivalent multimeric antibody CD19xCD16 related protein 2.

XX multivalent multimeric antibody; bispecific diabody; BsdB;  
 KW human B cell marker; CD19; human Fc gamma receptor III; CD16; cytostatic;  
 KW immunosuppressive; B-cell malignancy; non-Hodgkin lymphoma;  
 KW B-cell mediated autoimmune disease; B-cell depletion; immune response;  
 KW human anti-murine antibody response; CD19 x CD16 BsdB; PSKID19x16; mouse;  
 KW murine.

XX Mus musculus.

XX Key Location/Qualifiers  
 FH Region 31..35  
 FT /label= Complementarity\_determining\_region\_H1  
 FT Region 50..66  
 FT /label= Complementarity\_determining\_region\_H2  
 FT Region 99..106  
 FT /label= Complementarity\_determining\_region\_H3  
 FT Region 117..126  
 FT /label= Synthetic\_linker  
 FT Region 150..164  
 FT /label= Complementarity\_determining\_region\_L1  
 FT Region 180..186  
 FT /label= Complementarity\_determining\_region\_L2  
 FT Region 219..225  
 FT /label= Complementarity\_determining\_region\_L3  
 FT Region 247..257  
 FT /label= c-myc\_epitope  
 FT Region 259..264  
 FT /label= 6xHis\_tag

XX EP1314741-A1.

PD 28-MAY-2003.  
 XX 14-NOV-2001; 2001EP-00127061.  
 PF 14-NOV-2001; 2001EP-00127061.  
 XX 14-NOV-2001; 2001EP-00127061.  
 PR 14-NOV-2001; 2001EP-00127061.  
 XX (AFFI-) AFFIMED THERAPEUTICS AG.  
 XX Le Gall F, Kipriyanov MS, Moldenhauer G, Little M, Cochlovius B;  
 PI Schaefer JH;  
 XX WPI: 2003-620028/59.  
 DR N-PSDB; ADE29201.  
 XX Multivalent multimeric antibody for treating B-cell malignancies such as  
 PT non-Hodgkin lymphoma, comprises specificities, and antigen-binding domain  
 PT specific to human CD19 and CD16.  
 XX Example 1; SEQ ID NO 2; 38pp; English.

XX This invention relates to a novel multivalent multimeric antibody (a  
 CC bispecific diabody - BsdB) which comprises at least two binding sites  
 CC specific for the human B cell marker CD19 and human Fc gamma receptor III  
 CC (CD16). The invention may allow the development of compositions with  
 CC cytostatic or immunosuppressive activity. The antibody is useful for the  
 CC diagnosis and treatment of B-cell malignancies such as non-Hodgkin  
 CC lymphoma, B-cell mediated autoimmune diseases or the depletion of B-  
 CC cells. The multivalent multimeric antibody avoids the undesired immune  
 CC response such as human anti-murine antibody response. The specification  
 CC provides a process for stable high yield of recombinant antibodies. The  
 CC present sequence is that of a mature mouse derived protein encoded by the  
 CC DNA sequence of the CD19 x CD16 BsdB in the expression plasmid pSKID19x16  
 CC which was used in the exemplification of the invention.

XX Sequence 264 AA;

Query Match 80.4%; Score 1122; DB 7; Length 264;  
 Best Local Similarity 81.4%; Pred. No. 2e-74; Mismatches 14; Indels 4; Gaps 1;  
 Matches 215; Conservative 14;

QY 3 QVQLQSGAEELVRPQTSVKISCKASGYTFNFWLGVKQRPQGHLEWIGDIYPGGYTTNY 62  
 DB 1 QVQLQSGAEELVRPQTSVKISCKASGYTFNFWLGVKQRPQGHLEWIGDIYPGGYTTNY 60

QY 63 NEKFKGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVSSAKT 122  
 DB 61 NEKFKGKATVTADTSRTAYVQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVSSAKT 120

QY 123 TPKLGGDIELTQSPKFMSTSGDRVNTYKASQNV---GTNVAMFQKPGQSPKVLIIYS 178  
 DB 121 TPKLGGDILLTQTPASLAVSLGQRATISCKASQSDYDGDSTYLNWYQIIPGQPPKLLIYD 180

QY 179 ASYRYSGVDPDRFTSGSGTDFLTITISNVQSEDLAEYFCQYHTYPLTFGGGTGLEIKRAD 238  
 DB 181 ASNLVSGIIPRPSGSGTDFLTINHPVEKVDAAVTHCQSTEDPWTFTGGGTGLEIKRAD 240

QY 239 AAAAGSEQKLISEEDLNSHHHHHH 262  
 DB 241 AAAAGSEQKLISEEDLNSHHHHHH 264

RESULT 3

AAW58826  
 ID AAW58826 standard; protein; 248 AA.

XX AAW58826;

XX 18-AUG-1998 (first entry)

XX Human CD30 binding protein.

XX CD30 binding protein; human; suppressor; proliferation; metastasis;  
 KW tumour formation; CD30 antigen.

XX OS Homo sapiens.  
 XX PN DE19640733-A1.  
 XX PD 09-APR-1998.  
 XX PF 02-OCT-1996; 96DE-01040733.  
 XX PR 02-OCT-1996; 96DE-01040733.  
 XX PA (ABXE/) ABKEN H.  
 XX WI; 1998-218120/20.  
 XX DR N-PSDB; AAV11399.  
 XX PT Polypeptide than binds to CD30 without cell activation - for inhibiting  
 PT proliferation and metastasis of tumour cells, etc.  
 XX PS Claim 3; Page 7-8; 8pp; German.  
 XX CC This sequence represents a human CD30 binding protein which can be used  
 CC in a method for suppressing unchecked proliferation, tumour formation and  
 CC metastasis of cells expressing the CD30 antigen. This protein  
 CC specifically binds to CD30 without inducing cell activation by CD30. The  
 CC protein can also be used for probing, binding or enriching CD30-  
 CC expressing cells in vivo or in body fluids, cell suspensions or tissues  
 CC in vitro. A substance coupled to the protein accumulates in the vicinity  
 CC of CD30-expressing cells in vivo or in vitro  
 XX SQ Sequence 248 AA;

Query Match 71.8%; Score 1002; DB 2; Length 248;  
 Best Local Similarity 79.0%; Pred. No. 1.2e-65;  
 Matches 196; Conservative 12; Mismatches 28; Indels 12; Gaps 2;  
 QY 1 MAQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGWKORPGHLEWIGDIYPGGGYT 60  
 DB 1 MAQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGWKORPGHLEWIGDIYPGGGYT 60  
 QY 61 NYNEKFGKATVTADTSSRTAYQVRSLSLTSSEDSAVYFCARSASW-----YFDVWGARTT 114  
 DB 61 DYNQNFQKGTTLTADKSNATYMQLSLTSSEDSAVYFCARSADYGVETWYFAYWGGGTT 120  
 QY 115 VTSSAKTTPKLG-----DIETQSPKFMSTSGDRVNVYKASQNVGTNVAWFOQKP 168  
 DB 121 VTSSGG 180  
 QY 169 GQSPKVLIIYSASYRSGVDPDRFTGSGGTDFTLTISNVQSEDIAEYFCQYHYTPLTFGG 228  
 DB 181 GQSPKVLIIYSASYRSGVDPDRFTGSGGTDFTLTISNVQSEDIAEYFCQYHYTPLTFGG 240  
 QY 229 GTKLEIKR 236  
 DB 241 GTKLEIKR 248

RESULT 4  
 ABR57058  
 ID ABR57058 standard; protein; 562 AA.  
 XX AC ABR57058;  
 XX DT 05-AUG-2003 (first entry)  
 XX DE Plasmid pSKK2 scFv3-LL-Db19 amino acid sequence.

XX Multimeric single chain tandem Fv-antibody; antibacterial; virucide;  
 KW cytostatic; cytokine antagonist; diagnosis; viral disease; prion disease;  
 KW bacterial disease; tumoural disease; agglutination; red blood cell;  
 KW immune system; tumour cell; cytokine; cytotoxic.  
 OS Synthetic.

XX EP1293514-A1.  
 XX PD 19-MAR-2003.  
 XX PF 14-SEP-2001; 2001EP-00122104.  
 XX PR 14-SEP-2001; 2001EP-00122104.  
 XX PA (AFFI-) AFFIMED THERAPEUTICS AG.  
 XX PI Le Gall F, Kipriyanov S, Reusch U, Moldenhauer G, Little M;  
 XX WI; 2003-395536/38.  
 XX DR N-PSDB; ACC79606.  
 XX PT New multimeric Fv-antibody having monomers forming antigen-binding units  
 PT and sites, useful for the preparation of a pharmaceutical composition for  
 PT the treatment of a viral, bacterial, tumoral or prion diseases.  
 XX Example 1; Fig 6A-B; 29pp; English.  
 XX CC The present invention describes a multimeric Fv-antibody (I) comprising:  
 CC (a) monomers comprising at least 4 variable domains of which two  
 CC neighbouring domains of one monomer form an antigen-binding VH-VL or VL-  
 CC VH scFv unit; and/or (b) at least 2 variable domains of a monomer that  
 CC are non-covalently bound to 2 variable domains of another monomer  
 CC resulting in the formation of at least 2 additional antigen binding sites  
 CC to form multimerisation motif. Also described is a process for the  
 CC preparation of (I) comprising ligating DNA sequences encoding the peptide  
 CC linkers with the DNA sequences encoding the variable domains such that  
 CC the peptide linkers connect the variable domains of the multivalent  
 CC multimeric Fv-antibody, and expressing the DNA sequences encoding the  
 CC various monomers in an expression system. (I) has antibacterial, virucide  
 CC and cytostatic activities, and can be used as a cytokine antagonist. The  
 CC multimeric Fv-antibody is useful for diagnosis. The antibody can also be  
 CC used for the preparation of a pharmaceutical composition for the  
 CC treatment of a viral, bacterial, tumoural or prion disease, the  
 CC agglutination of red blood cells, linking cytotoxic cells of the immune  
 CC system to tumour cells, or linking activating cytokines, cytotoxic  
 CC substances or a protease to a target cell. The present sequence  
 CC represents the plasmid pSKK2 scFv3-LL-Db19 amino acid sequence, which is  
 CC used in the exemplification of the present invention

XX SQ Sequence 562 AA;

Query Match 67.8%; Score 946.5; DB 6; Length 562;  
 Best Local Similarity 68.0%; Pred. No. 3.5e-61;  
 Matches 185; Conservative 29; Mismatches 47; Indels 11; Gaps 3;  
 QY 2 AQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGWKORPGHLEWIGDIYPGGGYT 61  
 DB 291 SQVLOQSGAELVRPGTSVKISKASGYTFTNYLWGWKORPGHLEWIGDIYPGGGYT 350  
 QY 62 YNEKFGKATVTADTSSRTAYQVRSLSLTSSEDSAVYFCARSAS-----WYF--DVWGARTT 114  
 DB 351 YNGKFGKATVTADTSSRTAYQVRSLSLTSSEDSAVYFCARSADYGVETWYFAYWGGGTT 410  
 QY 115 VTSSAKTTPKLGDIETQSPKFMSTSGDRVNVYKASQNV-----GTNVAWFOQKP 170  
 DB 411 VTSSAKTTPKLGDIETQSPKFMSTSGDRVNVYKASQNV-----GTNVAWFOQKP 470  
 QY 171 SPKVLIIYSASYRSGVDPDRFTGSGGTDFTLTISNVQSEDIAEYFCQYHYTPLTFGGT 230  
 DB 471 PPKLLIYDAGNLVSGIPRFSGSGGTDFTLNIHPVKVDAAATVHCQSTEDPWFPGGT 530

QY 231 KLEIKRADAAGSEQKLISEDLNSHHHHH 262  
 DB 531 KLEIKRADAAGSEQKLISEDLNSHHHHH 562

RESULT 5



QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYF--DVMGART 113  
 DB 81 NYNGKFGKATLTADSSSTAYVQLSSLSLTSSEDSAVYFCARRETTVGRYYIANDYNGQT 140  
 QY 114 TTVSSAKTTPKLGDIELTQSPKFMSTSVGDRVNVITYKASQNVGNVAVFOOKPGOSPK 173  
 DB 141 SVTVSSAKTTPKLGDIELTQSPAINASAPGKVTWTCSSSV-SYMNWYQKSGTSPK 199  
 QY 174 VLYSASRYSGVDPDRFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPLTFTGGTKLE 233  
 DB 200 RWIYDTSKLAGVPAHFRGSGTSYSLTISGMEADAATYCCQWSSNPTFTGSGTKLE 259  
 QY 234 IKRADAAGSEQKLISEEDLNHHHHH 262  
 DB 260 INRADTAPTGEQKLISEEDLNHHHHH 288

RESULT 7  
 AAW82317  
 ID AAW82317 standard; protein; 288 AA.  
 XX AC AAW82317;  
 XX DT 26-FEB-1999 (first entry)  
 XX DE Mouse bispecific antibody variant OKT3/anti-CD19 protein.  
 XX KW OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;  
 KW organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19;  
 KW anti-CD3.  
 XX OS Mus sp.  
 XX OS Synthetic.  
 XX PN DE19721700-Cl.  
 XX PD 19-NOV-1998.  
 XX PF 23-MAY-1997; 97DE-01021700.  
 XX PR 23-MAY-1997; 97DE-01021700.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX PI Kipriyanov S, Little M, Moldenhauer G;  
 XX WPI; 1998-596150/51.  
 XX DR N-PSDB; AAV73337.  
 XX Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced  
 PT by another polar amino acid, useful for controlling transplant rejection,  
 PT and in tumour diagnostics and therapy.  
 XX FS Disclosure; Fig 3; 8pp; German.  
 XX CC This sequence represents a protein which has anti-CD19 activity and is  
 CC encoded by a monoclonal antibody (MAb) diabody derived from OKT3 with a  
 CC point-mutation where Cys at position H100A is replaced with another polar  
 CC amino acid, in this example Ser. The diabody encodes two OKT3 proteins,  
 CC one which has anti-CD19 activity and one with anti-CD3 activity. The MAb  
 CC is used in lowering or eliminating the transplant rejection in an organ  
 CC recipient and for diagnostic methods for tumours and tumour therapy  
 XX SQ Sequence 288 AA;  
 Query Match 67.1%; Score 936; DB 2; Length 288;  
 Best Local Similarity 69.0%; Pred. No. 1e-60;  
 Matches 185; Conservative 23; Mismatches 54; Indels 6; Gaps 2;

QY 1 MAQVLOQSGAELVPGTGVKISKASGYTFTNYLWGWKORPGHLEWIGDIYVGGYT 60  
 DB 21 MAQVLOQSGAELVPGTGVKISKASGYTFTNYLWGWKORPGHLEWIGDIYVPGSGYT 80

QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCAR--SASWYFDVMGARTTTVS 118  
 DB 81 NYNQKFKDKATLTADSSSTAYVQLSSLSLTSSEDSAVYFCARYDDHYSLDYWGQGTTLTVS 140  
 QY 119 SAKTTPKLGDIELTQSPKFMSTSVGDRVNVITYKASQNV-----GTNVAVFOOKPGOSPKV 174  
 DB 141 SAKTTPKLGDIELTQTPASLAVSLGORATISCKASQSDVDYDGDSYLNWYQQIPGQPPKL 200  
 QY 175 LIYSASRYSGVDPDRFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPLTFTGGTKLEI 234  
 DB 201 LIYDASNILVSGIPPRFSGSGTDFLTINHPVEKVDAAVTHCQOSTEDPWTFTGGTKLEI 260  
 QY 235 KRADAAAAGSEQKLISEEDLNHHHHH 262  
 DB 261 KRADAAAAGSEQKLISEEDLNHHHHH 288  
 RESULT 8  
 AAW82316  
 ID AAW82316 standard; protein; 288 AA.  
 XX AC AAW82316;  
 XX DT 26-FEB-1999 (first entry)  
 XX DE Mouse OKT3 variant antibody protein.  
 XX KW OKT3; monoclonal antibody; MAb; point mutation; transplant rejection;  
 KW organ recipient; diagnosis; tumour; therapy.  
 XX OS Mus sp.  
 XX OS Synthetic.  
 XX PN DE19721700-Cl.  
 XX PD 19-NOV-1998.  
 XX PF 23-MAY-1997; 97DE-01021700.  
 XX PR 23-MAY-1997; 97DE-01021700.  
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX PI Kipriyanov S, Little M, Moldenhauer G;  
 XX WPI; 1998-596150/51.  
 XX DR N-PSDB; AAV73335.  
 XX Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced  
 PT by another polar amino acid, useful for controlling transplant rejection,  
 PT and in tumour diagnostics and therapy.  
 XX FS Claim 3; Fig 2; 8pp; German.  
 XX CC This sequence represents a monoclonal antibody (MAb) derived from OKT3  
 CC with a point-mutation where Cys at position H100A is replaced with  
 CC another polar amino acid, in this example Ser. The MAb is used in  
 CC lowering or eliminating the transplant rejection in an organ recipient,  
 CC and for diagnostic methods for tumours and tumour therapy  
 XX SQ Sequence 288 AA;

Query Match 67.1%; Score 936; DB 2; Length 288;  
 Best Local Similarity 69.0%; Pred. No. 1e-60;  
 Matches 185; Conservative 23; Mismatches 54; Indels 6; Gaps 2;  
 QY 1 MAQVLOQSGAELVPGTGVKISKASGYTFTNYLWGWKORPGHLEWIGDIYVGGYT 60  
 DB 21 MAQVLOQSGAELVPGTGVKISKASGYTFTNYLWGWKORPGHLEWIGDIYVPGSGYT 80  
 QY 61 NYNEKFGKATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCAR--SASWYFDVMGARTTTVS 118

Db 81 NYNQKFKATLTDTTSSSTAYMQLSSLTSEDSAVVYCARYYDDHVSLDYWGQGTTLTYS 140  
 QY 119 SAKTTPKLGDIETQSPKFMSTSVGDRVNVVTKASQNV----GTNVAFQKPGQSPKV 174  
 Db 141 SAKTTPKLGDIILLTQTPASLAVSLGORATISCKASQSDVDYDGSYLNWYQIIPGQPPKL 200  
 QY 175 LIYSASYRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOQVHTYPLTFGGGTKLBI 234  
 Db 201 LIYDASNLVSGIPPRFSGSGGTDFTLNHPVEKVDAAATYHCQQSTEDPWTFFGGGTKLBI 260  
 QY 235 KRAADAAAGSEOKLISEEDLNHHHHH 262  
 Db 261 KRAADAAAGSEOKLISEEDLNHHHHH 288

## RESULT 9

AA50823  
 ID AAY50823 standard; protein; 539 AA.

XX AC AAY50823;

XX DT 18-FEB-2000 (first entry)

XX DE Fv-antibody construct containing antibody 9E10 epitope protein.

XX KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;

XX KW diagnosis; therapy; disease.

XX OS Synthetic.

XX PN DE19819846-A1.

XX PD 11-NOV-1999.

XX PF 05-MAY-1998; 98DE-01019846.

XX PR 05-MAY-1998; 98DE-01019846.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Little M, Kipriyanov S;

XX DR WPI; 2000-024472/03.

XX DR N-PSDB; AA243432.

XX PT Multivalent Fv-antibody constructs with at least four variable domains

XX PT connected by 1, 2 and 3 peptide linkers.

XX PS Example 1; Fig 6; 14pp; German.

XX CC This invention describes a novel multivalent Fv-antibody construct with  
 CC at least four variable domains that are connected to one another by 1, 2  
 CC and 3 peptide linkers. The construct has antiviral, antibacterial and  
 CC cytostatic activity. The multivalent Fv-antibody constructs are useful  
 CC for the diagnosis and/or therapy of disease, especially viral, bacterial  
 CC or tumor diseases. The multivalent Fv-antibody constructs have increased  
 CC stability when in the form of a single chain dimer. This sequence  
 CC represents a tetravalent Fv antibody construct composed of the antibody  
 CC 9E10 epitope in expression plasmid pDISC3x19-SL

XX SQ Sequence 539 AA;

Query Match 66.7%; Score 930; DB 3; Length 539;  
 Best Local Similarity 67.5%; Pred. No. 5.4e-60;  
 Matches 181; Conservative 28; Mismatches 51; Indels 8; Gaps 3;  
 QY 2 AQVQLQSQGAELVRPGTSVKISKASGYFTNTWLGWVKQRPQGHLEWIGDIYPGGGYTN 61  
 Db 273 SQVQLQSQGAELVRPGTSVKISKASGYAFSSYMNWVKQRPQGHLEWIGDIYPGGGYTN 332  
 QY 62 YNEKFKGKATVTADTSSRTAYVQVRSITSEDSAVVFCARSAS-----WYF--DVMGARTT 114  
 Db 333 YNGKFKGKATLTADSSSTAYMQLSSLTSEDSAVVFCARRETTVGRYYIAMDYWGQGT 392

QY 115 VTVSSAKTTPKLGDIETQSPKFMSTSVGDRVNVVTKASQNVGTNVAFQKPGQSPKV 174  
 Db 393 VTVSSAKTTPKLGDIIVLTQSPAIMSAPGEKVTWMTCSASSSV-SYMNWYQKSGTSPKR 451  
 QY 175 LIYSASYRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQOQVHTYPLTFGGGTKLBI 234  
 Db 452 WIYDTSKLASGVPAIFRSGSGTSYSLTISGMEADAATYYCQWSSNPFTFGSGTKLBI 511  
 QY 235 KRAADAAAGSEOKLISEEDLNHHHHH 262  
 Db 512 NEADTAPTGSEQKLISEEDLNHHHHH 539

## RESULT 10

AA50822

ID AAY50822 standard; protein; 554 AA.

XX AC AAY50822;

XX DT 18-FEB-2000 (first entry)

XX DE Fv-antibody construct containing antibody 9E10 epitope protein.

XX KW Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;

XX KW diagnosis; therapy; disease.

XX OS Synthetic.

XX PN DE19819846-A1.

XX PD 11-NOV-1999.

XX PF 05-MAY-1998; 98DE-01019846.

XX PR 05-MAY-1998; 98DE-01019846.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Little M, Kipriyanov S;

XX DR WPI; 2000-024472/03.

XX DR N-PSDB; AA243431.

XX PT Multivalent Fv-antibody constructs with at least four variable domains

XX PT connected by 1, 2 and 3 peptide linkers.

XX PS Example 1; Fig 5; 14pp; German.

XX CC This invention describes a novel multivalent Fv-antibody construct with  
 CC at least four variable domains that are connected to one another by 1, 2  
 CC and 3 peptide linkers. The construct has antiviral, antibacterial and  
 CC cytostatic activity. The multivalent Fv-antibody constructs are useful  
 CC for the diagnosis and/or therapy of disease, especially viral, bacterial  
 CC or tumor diseases. The multivalent Fv-antibody constructs have increased  
 CC stability when in the form of a single chain dimer. This sequence  
 CC represents a bivalent Fv antibody construct composed of the antibody 9E10  
 CC epitope in expression plasmid pDISC3x19-LL

XX SQ Sequence 554 AA;

Query Match 66.7%; Score 930; DB 3; Length 554;  
 Best Local Similarity 67.5%; Pred. No. 5.6e-60;  
 Matches 181; Conservative 28; Mismatches 51; Indels 8; Gaps 3;  
 QY 2 AQVQLQSQGAELVRPGTSVKISKASGYFTNTWLGWVKQRPQGHLEWIGDIYPGGGYTN 61  
 Db 289 SQVQLQSQGAELVRPGTSVKISKASGYAFSSYMNWVKQRPQGHLEWIGDIYPGGGYTN 347  
 QY 62 YNEKFKGKATVTADTSSRTAYVQVRSITSEDSAVVFCARSAS-----WYF--DVMGARTT 114  
 Db 348 YNGKFKGKATLTADSSSTAYMQLSSLTSEDSAVVFCARRETTVGRYYIAMDYWGQGT 407



XX SQ Sequence 283 AA;  
Query Match 65.8%; Score 917.5; DB 8; Length 283;  
Best Local Similarity 69.4%; Pred. No. 2.2e-59;  
Matches 186; Conservative 21; Mismatches 50; Indels 11; Gaps 3;  
QY 1 MAQVQLQSGAEIVRGTSVKISKASGYFTNYWLGWYKQRPCHGLEWIGDIYPCGGYT 60  
DB 21 MAQVQLQSGPELVKFGASVMSCKASGYFTSYNMHWYKQRPQGQGLEWIGYVNPYNDGI 80  
QY 61 NYNEKFKGKATVTADTSSTAYVQVRSLSSEDSAVYFCARSASWYFDVMGARTTIVTSSA 120  
DB 81 NYNEKFKGKATLSDSKSSATAYMELSLTSDSASVYFCARKG---LDYWGQGGTTVTSSG 137  
QY 121 KTPPKLGG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGTVNAVFQKPGQSPKV 174  
DB 138 GGSASGGGGGGGGDIELTQSPKFMSTSVGDRVSVTCKASQFVGTVMVYQKPGQSPKA 197  
QY 175 LIYSASYRYSGVDPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQOYHTYPLTFGGGTKLEI 234  
DB 198 LIYSASTRTGVPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQYSSPYTFGSGTKLEI 257  
QY 235 KRADAAAAGSEQKLISEEDLNHHHHH 262  
DB 258 KRAAGAPVPYDPDL--EPRAAHHHHH 283

RESULT 13  
ADR70320  
ID ADR70320 standard; protein; 267 AA.  
XX AC ADR70320;  
XX DT 18-NOV-2004 (first entry)  
XX DE Poliovirus receptor (PVR)-specific scFv2 protein.  
XX KW poliovirus receptor; PVR; CD155; cluster of differentiation 155;  
KW receptor mediated adhesion modulation;  
KW cell trafficking behaviour modulation;  
KW cell invasion behaviour modulation; proliferative disorder; cancer;  
KW metastasis; PVR-mediated adhesion; PVR-mediated invasion potential;  
KW scFv2.  
XX OS Unidentified.  
XX PN WO2004074324-A2.  
XX PD 02-SEP-2004.  
XX PF 19-FEB-2004; 2004WO-EP001637.  
XX PR 24-FEB-2003; 2003US-0450064P.  
XX PR 28-MAY-2003; 2003EP-00012314.  
XX PA (XERI-) XERION PHARM AG.  
XX PA (TUFT ) UNIV TUFTS.  
XX PI Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Jay DG;  
PI Eustace BK, Sloan KE;  
XX DR N-PSDB; ADR70322.  
XX DR WPI; 2004-652917/63.  
XX XX New molecules that modulate poliovirus receptor (PVR) mediated adhesion,  
PT trafficking and/or invasion behavior of a cell expressing CD155 or PVR,  
PT useful for preventing or treating proliferative disorders, such as  
PT cancer.  
XX XX Claim 7; SEQ ID NO 4; 87pp; English.  
XX XX The invention comprises molecules that specifically bind to at least one

CC intra- or extracellular domain of the poliovirus receptor (PVR) - also  
CC known as CD155 (cluster of differentiation 155). The molecules of the  
CC invention have the ability to modulate receptor mediated adhesion,  
CC trafficking and/or invasion behaviour of a cell expressing PVR. The  
CC molecules of the invention are useful for the prevention and/or treatment  
CC of proliferative disorders, cancer or metastasis. The molecules of the  
CC invention are also useful for identifying agents that can modulate PVR-  
CC mediated adhesion or invasion potential of cells. The present amino acid  
CC sequence represents a PVR-specific scFv protein of the invention.  
XX SQ Sequence 267 AA;  
Query Match 65.3%; Score 911.5; DB 8; Length 267;  
Best Local Similarity 72.8%; Pred. No. 5.8e-59;  
Matches 182; Conservative 19; Mismatches 32; Indels 17; Gaps 4;  
QY 5 QLQSGAEIVRGTSVKISKASGYFTNYWLGWYKQRPCHGLEWIGDIYPCGGYTNVNE 64  
DB 1 QLQSGPELVKFGASVKISCKTSGYFTFYTMHWYKQSHGKSLWIGIHPPNGDTSYNG 60  
QY 65 KFKGKATVTADTSSTAYVQVRSLSSEDSAVYFCARSASWY--FDVWGARTTIVTSSAKT 122  
DB 61 RFKKGATLTVDKSSSTAYMELSLTSEDSAVYFCAR---WTGDFDYWGQGTTLTIVTSGG 117  
QY 123 TPKLGG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGTVNAVFQKPGQSPKV 174  
DB 118 GSGGGGGGGGGGALDIVMTQSPKFMSTSVGDRVSVTCKASQNVGTVNAVYQKPGQSPKA 177  
QY 175 LIYSASYRYSGVDPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQOYHTYPLTFGGGTKLEI 234  
DB 178 LIYSASYRYSGVDPDRFTGSGSGTDFLTITSNVQSEDLAEYFCQYNSPYTFGGGTKLEI 237  
QY 235 KRADAAAAGS 244  
DB 238 K----AAAGA 243  
RESULT 14  
ADP84954  
ID ADP84954 standard; protein; 267 AA.  
XX AC ADP84954;  
XX DT 09-SEP-2004 (first entry)  
XX DE Single chain Fv fragment SEQ ID NO 96.  
XX KW antibody; Core-1 antigen; framework region; immunoglobulin superfamily;  
KW protease inhibitor; lectin; helix-bundle protein; lipocalin;  
KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;  
KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;  
KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;  
XX OS Unidentified.  
XX PN WO2004050707-A2.  
XX PD 17-JUN-2004.  
XX PF 01-DEC-2003; 2003WO-DE003994.  
XX PR 29-NOV-2002; 2002DE-01056900.  
XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.  
XX PI Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;  
PI Christensen PA;  
XX DR WPI; 2004-461095/43.  
XX XX New recognition molecules, e.g. antibodies (and nucleic acids) that bind  
PT specifically to Core-1 antigens, useful for diagnosis, treatment and



prevention of tumors and metastases.  
 Claim 26; SEQ ID NO 96; 136pp; German.  
 This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IGM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, and/or monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.  
 Sequence 267 AA;  
 Query Match 65.2%; Score 909.5; DB 8; Length 267;  
 Best Local Similarity 66.5%; Pred. No. 8.1e-59;  
 Matches 179; Conservative 29; Mismatches 40; Indels 21; Gaps 4;  
 QY 3 QVQLQQSGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 62  
 Db 1 QVQLKESGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 60  
 QY 63 NEKFKGATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDV-----WGARTTV 115  
 Db 61 NEKFKGATLTADTSSSTAYWQLSSLTSEDSAVYFCA-----YYDAAGPGFAYWGQGT 115  
 QY 116 TVSSAKTTPKLGDIETQSPKFMSTSGVDRVNTYKASQNV-----GTNVANFQPKPG 170  
 Db 116 TVSSASGSGSSADIQMTQTPSLPVLGPDQASISCRSSQSIHNSNGNTYLEWYLPKPG 175  
 QY 171 SPKVLIIYSASRYSGVDPRTFGSGGDTFTLTISNVOSEDLAIEYFCQYHYPLTFGGGT 230  
 Db 176 SPKLLIYKSNRFGVDPRTFGSGGDTFTLKIRVEAEDLGVIYFCQGHVPTFGGT 235  
 QY 231 KLEIKRADA-----AAAGSEQKLISEEDLN 255  
 Db 236 KLEIKRAAHHHHHGAEGKLISEEDLN 264  
 RESULT 15  
 ADP84957  
 ID ADP84957 standard; protein; 264 AA.  
 AC ADP84957;  
 XX  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 XX Single chain Fv fragment SEQ ID NO 99.  
 XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;  
 KW protease inhibitor; lectin; helix-bundle protein; lipocalin;  
 KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;  
 KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;  
 KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;  
 KW metastasis.  
 XX Unidentified.  
 XX WO2004050707-A2.  
 XX 17-JUN-2004.  
 XX 01-DEC-2003; 2003WO-DE003994.  
 XX 29-NOV-2002; 2002DE-01056900.  
 XX (NEMO-) NEMOD BIOTHEAPEUTICS GMBH & CO KG.  
 XX Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;  
 PI Christensen PA;  
 XX WPI; 2004-461095/43.  
 PS Claim 26; SEQ ID NO 99; 136pp; German.  
 CC This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IGM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, and/or monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.  
 Sequence 267 AA;  
 Query Match 65.2%; Score 909.5; DB 8; Length 267;  
 Best Local Similarity 66.5%; Pred. No. 8.1e-59;  
 Matches 179; Conservative 29; Mismatches 40; Indels 21; Gaps 4;  
 QY 3 QVQLQQSGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 62  
 Db 1 QVQLKESGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 60  
 QY 63 NEKFKGATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDV-----WGARTTV 115  
 Db 61 NEKFKGATLTADTSSSTAYWQLSSLTSEDSAVYFCA-----YYDAAGPGFAYWGQGT 115  
 QY 116 TVSSAKTTPKLGDIETQSPKFMSTSGVDRVNTYKASQNV-----GTNVANFQPKPG 170  
 Db 116 TVSSASGSGSSADIQMTQTPSLPVLGPDQASISCRSSQSIHNSNGNTYLEWYLPKPG 175  
 QY 171 SPKVLIIYSASRYSGVDPRTFGSGGDTFTLTISNVOSEDLAIEYFCQYHYPLTFGGGT 230  
 Db 176 SPKLLIYKSNRFGVDPRTFGSGGDTFTLKIRVEAEDLGVIYFCQGHVPTFGGT 235  
 QY 231 KLEIKRADA-----AAAGSEQKLISEEDLN 255  
 Db 236 KLEIKRAAHHHHHGAEGKLISEEDLN 264  
 RESULT 15  
 ADP84957  
 ID ADP84957 standard; protein; 264 AA.  
 AC ADP84957;  
 XX  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 XX Single chain Fv fragment SEQ ID NO 99.  
 XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;  
 KW protease inhibitor; lectin; helix-bundle protein; lipocalin;  
 KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;  
 KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;  
 KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;  
 KW metastasis.  
 XX Unidentified.  
 XX WO2004050707-A2.  
 XX 17-JUN-2004.  
 XX 01-DEC-2003; 2003WO-DE003994.  
 XX 29-NOV-2002; 2002DE-01056900.  
 XX (NEMO-) NEMOD BIOTHEAPEUTICS GMBH & CO KG.  
 XX Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;  
 PI Christensen PA;  
 XX WPI; 2004-461095/43.  
 PS Claim 26; SEQ ID NO 99; 136pp; German.  
 CC This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IGM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, and/or monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.  
 Sequence 267 AA;  
 Query Match 65.2%; Score 909.5; DB 8; Length 267;  
 Best Local Similarity 66.5%; Pred. No. 8.1e-59;  
 Matches 179; Conservative 29; Mismatches 40; Indels 21; Gaps 4;  
 QY 3 QVQLQQSGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 62  
 Db 1 QVQLKESGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 60  
 QY 63 NEKFKGATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDV-----WGARTTV 115  
 Db 61 NEKFKGATLTADTSSSTAYWQLSSLTSEDSAVYFCA-----YYDAAGPGFAYWGQGT 115  
 QY 116 TVSSAKTTPKLGDIETQSPKFMSTSGVDRVNTYKASQNV-----GTNVANFQPKPG 170  
 Db 116 TVSSASGSGSSADIQMTQTPSLPVLGPDQASISCRSSQSIHNSNGNTYLEWYLPKPG 175  
 QY 171 SPKVLIIYSASRYSGVDPRTFGSGGDTFTLTISNVOSEDLAIEYFCQYHYPLTFGGGT 230  
 Db 176 SPKLLIYKSNRFGVDPRTFGSGGDTFTLKIRVEAEDLGVIYFCQGHVPTFGGT 235  
 QY 231 KLEIKRADA-----AAAGSEQKLISEEDLN 255  
 Db 236 KLEIKRAAHHHHHGAEGKLISEEDLN 264  
 RESULT 15  
 ADP84957  
 ID ADP84957 standard; protein; 264 AA.  
 AC ADP84957;  
 XX  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 XX Single chain Fv fragment SEQ ID NO 99.  
 XX antibody; Core-1 antigen; framework region; immunoglobulin superfamily;  
 KW protease inhibitor; lectin; helix-bundle protein; lipocalin;  
 KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;  
 KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;  
 KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;  
 KW metastasis.  
 XX Unidentified.  
 XX WO2004050707-A2.  
 XX 17-JUN-2004.  
 XX 01-DEC-2003; 2003WO-DE003994.  
 XX 29-NOV-2002; 2002DE-01056900.  
 XX (NEMO-) NEMOD BIOTHEAPEUTICS GMBH & CO KG.  
 XX Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;  
 PI Christensen PA;  
 XX WPI; 2004-461095/43.  
 PS Claim 26; SEQ ID NO 99; 136pp; German.  
 CC This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified sequences, especially where the framework regions are from the immunoglobulin (Ig) superfamily, protease inhibitors, lectins, helix-bundle proteins and/or lipocalins. Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IGM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, and/or monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.  
 Sequence 264 AA;  
 Query Match 64.9%; Score 906; DB 8; Length 264;  
 Best Local Similarity 66.5%; Pred. No. 1.5e-56;  
 Matches 179; Conservative 30; Mismatches 36; Indels 24; Gaps 5;  
 QY 3 QVQLQQSGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 62  
 Db 1 QVQLKESGAELVRPGTSVKISCKASGYTFNFWLWGWKQRPFGHGLEWIGDIYPGGYTN 60  
 QY 63 NEKFKGATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDV-----WGARTTV 115  
 Db 61 NEKFKGATLTADTSSSTAYWQLSSLTSEDSAVYFCA-----YYDAAGPGFAYWGQGT 115

Qy	116	TVSSAKTPEKLGDIETQSPKFMSTSVGDRVNVITYKASQNV-----GTNVAVFOQKPGQ	170
Db	116	TVSSASS--SADIQMTQPLSLPVSIGDQASISCRSSQSIHNSNGNTYLEWYLOKPGQ	172
Qy	171	SPKVLISASRYSGVDPDRFTSGSGGTDFTLTISNVQSEDLAEYFCQQYHTYPLTFGGGT	230
Db	173	SPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGVYYCFQSGSHVPTTFGGGT	232
Qy	231	KLEIKRADA-----AAGSEQKLISEEDLN	255
Db	233	KLEIKRAAAHHHHHHGAAEQKLISEEDLN	261

Search completed: February 9, 2006, 03:27:46  
Job time : 275.825 secs

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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:28:13 ; Search time 25.4654 Seconds  
(without alignments)  
989.922 Million cell updates/sec

Title: US-10-049-404-2  
Perfect score: 1395  
Sequence: 1 MAQVQLQSGAEIVRPGETSV.....GSEQKLISEDLNHHHHH 262

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	708	50.8	268	A56446	Ig heavy chain V r
2	664.5	47.6	249	S41374	single chain Fv an
3	583.5	41.8	233	JCS322	p53 specific singl
4	530.5	37.3	141	A39276	Ig heavy chain pre
5	516	37.0	121	GWMS11	Ig heavy chain V r
6	501	35.9	115	A56700	Ig heavy chain (an
7	497	35.6	246	S38950	Ig gamma chain - m
8	496	35.6	446	S40295	Ig gamma-2a chain
9	489	35.1	128	A47159	Ig kappa chain V r
10	489	35.1	128	A47159	Ig lambda chain V
11	486	34.8	119	PL0089	Ig heavy chain V r
12	486	34.8	136	PL0208	Ig heavy chain pre
13	484	34.7	123	E30560	Ig heavy chain V r
14	482	34.6	119	PL0086	Ig heavy chain V r
15	480	34.4	107	B28195	Ig kappa chain V r
16	478	34.3	108	PL0204	anti-DNA autoantib
17	476	34.1	119	PL0085	Ig heavy chain V r
18	475	34.1	140	PH1482	Ig heavy chain V r
19	472	33.8	117	S42466	Ig kappa chain V r
20	471.5	33.8	116	S53751	antibody Fab Jel 1
21	468.5	33.6	214	PC4202	monoclonal antibod
22	468	33.5	118	S38565	Ig heavy chain V r
23	468	33.5	119	C30562	Ig heavy chain V r
24	467.5	33.5	108	B44371	Ig kappa chain V r
25	467	33.5	138	E32513	Ig heavy chain pre
26	467	33.5	140	T01407	Ig heavy chain (my
27	466	33.4	119	C30562	Ig heavy chain V r
28	464.5	33.3	469	S27483	Ig gamma-2a chain
29	464	33.3	117	MMMS4E	Ig heavy chain V r

30	463	33.2	117	1	MMMSJ5	Ig heavy chain V r
31	463	33.2	119	2	D30562	Ig heavy chain V r
32	462	33.1	118	2	A24754	Ig heavy chain V r
33	462	33.1	149	1	KVMS11	Ig kappa chain pre
34	460	33.0	144	2	B30502	Ig heavy chain V r
35	459	32.9	116	2	S20645	Ig heavy chain V r
36	459	32.9	140	1	HVMSG7	Ig heavy chain pre
37	459	32.9	140	2	PH1484	Ig heavy chain V r
38	458	32.8	140	2	PH1489	Ig heavy chain V r
39	457	32.8	121	2	PL0281	Ig heavy chain V r
40	457	32.8	131	2	PL0207	anti-idiotypic ant
41	457	32.8	140	2	PH1488	Ig heavy chain V r
42	455	32.6	98	2	PH1072	Ig light chain V r
43	455	32.6	124	2	S06824	Ig heavy chain V r
44	453.5	32.5	106	2	PH1002	Ig heavy chain V r
45	453.5	32.5	120	2	B22769	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C;Species: Mus musculus (house mouse)

C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C;Accession: A56446

R;Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A;Reference number: A56446; MUID:95229583; PMID:7713873

A;Accession: A56446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <FAN>

A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 50.8%; Score 708; DB 2; Length 268;

Best Local Similarity 54.3%; Pred. No. 2e-44;

Matches 146; Conservative 41; Mismatches 64; Indels 18; Gaps 5;

QY	1	MAQVQLQSGAEIVRPGETSVKISKASGYTFTNYLWGWKQRPQGHGLEWIDYIPGGGYT	60
DB	1	MAQVQLQSGAEIVKPGASVKLSCTTSQFNKDTYMHVWQRPQGLEWIGRIAPANGIT	60
QY	61	NYNEKFKGKATVTADTSSRTAYVQVRSLSLTSQSAVYFCARSASWYF----	116
DB	61	KYDPKFGKATIAADTSSNTAYLQLSLTSEDYAVYVC--ASYYLTRYENYWGQGTFTV	117
QY	117	VSS-----AKTTPKLGSDIELTQSPKFMSTSGVDRVNVYKASQNVGTNVAVFQKPGQ	170
DB	118	VSSGGSGSGSGGGGGSDIELTQSPAIMASLGEKVTMSCRASSSNVNF-IYWTQQKSDA	176
QY	171	SPKVIYASRYSGVDPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQOYHTYPTFGGGT	230
DB	177	SPKLWYVTYSHLPGPVPAREFGSGSGSNYSLTISMEGEDAATYTCQOPTSSPTFGSGT	236
QY	231	KLEIKRADA-----AAGSEQKLISEEDLN	255
DB	237	KLEIKRSAHHHHHHGAAEQKLISEEDLN	265

RESULT 2

S41374

single chain Fv antibody - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C;Accession: S41374

R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A;Description: Construction and functional characterization of a single chain Fv antib

A;Reference number: S41374



Db 121 S 121

## RESULT 6

A56700  
Ig heavy chain (antibody 93-6) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 17-Mar-1999  
C:Accession: A56700  
R;Ge, L.; Lupas, A.; Peraldi-Roux, S.; Spada, S.; Plueckthun, A.  
J. Biol. Chem. 270, 12446-12451, 1995  
A:Reference number: A56700; MUID:95279369; PMID:7759486  
A:Accession: A56700  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-115 <GBA>  
A:Cross-references: UNIPARC:UPI0000176E41; GB:Z48768  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 35.9%; Score 501; DB 2; Length 115;

Best Local Similarity 78.6%; Pred. No. 8.5e-30;

Matches 92; Conservative 13; Mismatches 10; Indels 2; Gaps 1;

Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNFWLGNWVKQRPCHGLEWIGDIYPCGGYTNV 62

Db 1 EVKLVSQAEIVRPGTSVKISKASGYFTNFWLGNWVKQRPCHGLEWIGDIYPCGGYPNY 60

Qy 63 NEKFKGKATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDVWGARTTIVTSS 119

Db 61 NEKFKGKATLTADTSSRTAYVQVRLTSEDSAVYFCARS--VPDYGQGTTLIVSS 115

## RESULT 7

S38950  
Ig gamma chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S38950  
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Froesch, M.; Weisgerber, C.; Bol  
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993  
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha  
A:Reference number: S38950; MUID:94128242; PMID:8297501  
A:Accession: S38950  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-246 <KLE>  
A:Cross-references: UNIPARC:UPI0000176F3B  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 35.6%; Score 497; DB 2; Length 246;

Best Local Similarity 49.2%; Pred. No. 4e-29;

Matches 119; Conservative 24; Mismatches 61; Indels 38; Gaps 8;

Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNFWLGNWVKQRPCHGLEWIGDIYPCGGYTNV 62

Db 1 QIQLQSGPELVRFPGASVKISKASGYFTDYIHWVKQRPCHGLEWIGIYPCGSGNTKY 60

Qy 63 NEKFKGKATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDVWGARTTIVTSSAKT 122

Db 61 NEKFKGKATLTVDTSSTAYMQLSSTSEDSAVYFCARGGKPFAMDYGQGTSTVTSSAKT 120

Qy 123 TPQLGGDIELTQSPKFMSTSVGDRVNVYKASQNVGTVN-AWFOQKPGQSPKVLIIYSASY 181

Db 121 T-----APSVYPLAPVCGD-----TTGSSVTILGCLVKGYPF-----PVTLTWNSGS 162

Qy 182 RYSGV-----PDRFTGSGSGTDFTLTISNVQSEDLAEYFCQOQHYTYPLTFGGGKTLE 233

Db 163 LSSGVHFTPAVLQSDLYTLSSS---VTVTSSTWPSQSIT---CNVAHP-----ASSTKVD 211

Qy 234 IK 235

Db 212 KK 213

## RESULT 8

S40295  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C:Accession: S40295  
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Froesch, M.; Weisgerber, C.; B  
submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
A:Cross-references: UNIPROT:Q99L25; UNIPARC:UPI0000176F38  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 35.6%; Score 497; DB 2; Length 446;

Best Local Similarity 49.2%; Pred. No. 8e-29;

Matches 119; Conservative 24; Mismatches 61; Indels 38; Gaps 8;

Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNFWLGNWVKQRPCHGLEWIGDIYPCGGYTNV 62

Db 1 QIQLQSGPELVRFPGASVKISKASGYFTDYIHWVKQRPCHGLEWIGIYPCGSGNTKY 60

Qy 63 NEKFKGKATVTADTSSRTAYVQVRLTSEDSAVYFCARSASWYFDVWGARTTIVTSSAKT 122

Db 61 NEKFKGKATLTVDTSSTAYMQLSSTSEDSAVYFCARGGKPFAMDYGQGTSTVTSSAKT 120

Qy 123 TPQLGGDIELTQSPKFMSTSVGDRVNVYKASQNVGTVN-AWFOQKPGQSPKVLIIYSASY 181

Db 121 T-----APSVYPLAPVCGD-----TTGSSVTILGCLVKGYPF-----PVTLTWNSGS 162

Qy 182 RYSGV-----PDRFTGSGSGTDFTLTISNVQSEDLAEYFCQOQHYTYPLTFGGGKTLE 233

Db 163 LSSGVHFTPAVLQSDLYTLSSS---VTVTSSTWPSQSIT---CNVAHP-----ASSTKVD 211

Qy 234 IK 235

Db 212 KK 213

## RESULT 9

A28195  
Ig kappa chain V region (anti-haloperidol antibody A) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Dec-1999 #sequence\_revision 01-Dec-1989 #text\_change 21-Jan-2000  
C:Accession: A28195  
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid  
A:Reference number: A28195; MUID:88153717; PMID:3267217

A;Accession: A28195  
A:Molecule type: mRNA  
A;Residues: 1-107 <SHE>  
A;Cross-references: UNIPARC:UPI0000114D69; GB:M19766; NID:gl97039; PIDN:AAA38891.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 35.6%; Score 496; DB 2; Length 107;  
Best Local Similarity 88.8%; Pred. No. 1.8e-29;  
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 129 DIETLQSPKFMSTSGVDRVNVYKASQNGVTNVAFQKPGQSPKVIYISASRYSGVDP 188  
DB 1 DILMTQSKFMSTSGVDRVSVTKASQNGVGNVAMHQKPGQSPKALIYSASRYSGVDP 60

QY 189 RFTGSGSGTDFLTITISNVQSEDLAEYFCQYHTYPLTFGGGTKLEIK 235  
DB 61 RFTGSGSGTDFLTITINVSQSEDLAEYFCQYNSYPTFGGGTKLEIK 107

RESULT 10  
A47159  
Ig lambda chain V region (CEA-specific maId T84.66) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: A47159  
R;Gaidd, P.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.  
J. Biol. Chem. 268, 14138-14145, 1993  
A;Title: Molecular characterization of a cloned idiotype cascade containing a network a  
A;Reference number: A47159; MUID:93300804; PMID:7686150  
A;Accession: A47159  
A;Status: preliminary  
A:Molecule type: DNA; protein  
A;Residues: 1-128 <GAI>  
A;Cross-references: UNIPARC:UPI00001767A5  
A;Experimental source: hybridoma 6G6.C4  
A;Note: sequence extracted from NCBI backbone (NCBI:134419, NCBI:134420)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 35.1%; Score 489; DB 2; Length 128;  
Best Local Similarity 86.2%; Pred. No. 7.1e-29;  
Matches 94; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 128 GDIELTQSPKFMSTSGVDRVNVYKASQNGVTNVAFQKPGQSPKVIYISASRYSGVP 187  
DB 20 GDIVLQSKFMSTSGVDRVSVTKASQNGVGNVAMVYQKPGQSPKALIYSASRYSGVP 79

QY 188 DFTGSGSGTDFLTITISNVQSEDLAEYFCQYHTYPLTFGGGTKLEIKR 236  
DB 80 DFTGSGSGTDFLTITISNVQSEDLAEYFCQYDYNPWTFGGGTKLEIKR 128

RESULT 11  
PL0089  
Ig heavy chain V region (12S18-1) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Mar-2000  
C;Accession: PL0089  
R;Week, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1989  
A;Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are  
A;Reference number: PL0080; MUID:89094248; PMID:2492056  
A;Accession: PL0089  
A:Molecule type: mRNA  
A;Residues: 1-119 <MEE>  
A;Cross-references: UNIPARC:UPI0000115F1B; GB:X58580; GB:Y00794; NID:g51591; PIDN:CAA414  
A;Note: the sequence shown here is from the VH region of an antidiotypic monoclonal ant  
A;Note: the sequences from two other clones (18S28-16 and 12S84-3) were almost identical to  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.8%; Score 486; DB 2; Length 119;  
Best Local Similarity 73.9%; Pred. No. 1.1e-28;  
Matches 88; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 3 QVLOQSGAELVRPGTSVKISCKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGYYTNY 62  
DB 1 QVLOQPGAELVRPGTSVKISCKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGYYTNY 60

QY 63 NEKFKGKATVTADTSRTAYVQVRLTSEDSSAVYFCARSA--SWYFDVMGARTTIVTVSS 119  
DB 61 NEKFKSKATLTVDTSSTAYMQISLTSEDSSAVYFCARNEGAVYFDVWGXGTTVAXSS 119

RESULT 12  
PL0208  
Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c)  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 13-Feb-1998  
C;Accession: PL0208  
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.  
Mol. Immunol. 27, 429-433, 1990  
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reacti  
A;Reference number: PL0207; MUID:90309764; PMID:1973259  
A;Accession: PL0208  
A:Molecule type: mRNA  
A;Residues: 1-136 <SOU>  
A;Cross-references: UNIPARC:UPI0000176C6F  
A;Experimental source: hybridoma cell E225  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;50-54/Region: complementarity-determining 1  
F;69-85/Region: complementarity-determining 2  
F;118-125/Region: complementarity-determining 3  
F;118-121/Region: D region  
F;122-136/Region: JH region

Query Match 34.8%; Score 486; DB 2; Length 136;  
Best Local Similarity 74.6%; Pred. No. 1.3e-28;  
Matches 88; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 2 AVOVLQSGAELVRPGTSVKISCKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGYYTNY 61  
DB 19 SOVLQPGSELVRPGTSVKISCKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGSDSN 78

QY 62 YNEKFKGKATVTADTSRTAYVQVRLTSEDSSAVYFCARSAWYFDVWGARTTIVTVSS 119  
DB 79 YDEKFKSKATLTVDTSSTAYMQISLTSEDSSAVYFCARGLAFYFDHWGQGITLTIVSS 136

RESULT 13  
B30560  
Ig heavy chain V region (28.4.10A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 23-Jul-1999  
C;Accession: B30560  
R;Matsuda, T.; Kabat, E.A.  
J. Immunol. 142, 863-870, 1989  
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon  
A;Reference number: A30560; MUID:89110062; PMID:2464028  
A;Accession: B30560  
A;Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-123 <MAT>  
A;Cross-references: UNIPARC:UPI0000114E20; GB:M24269; NID:gl95619; PIDN:AAA38373.1; PID:  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 34.7%; Score 484; DB 2; Length 123;

Best Local Similarity 77.2%; Pred. No. 1.6e-28;  
Matches 95; Conservative 7; Mismatches 15; Indels 6; Gaps 1;  
QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNFWLGVKQRPGLGLEWIGDIYPGGGYTN 62  
Db 1 QVQLQSGAELVRPGTSVKISCKASGYTFNFWLGVKQRPGLGLEWIGDIYPGGGYTN 60  
QY 63 NEKFKGKATVTADTSSRTAVQVRSITSEDSAVYFCARSAS-----WYFDVWGARTT 116  
Db 61 NEKFKGKATVTADTSSRTAVQVRSITSEDSAVYFCARSASPYDYGWYFDVWGARTT 120  
QY 117 VSS 119  
Db 121 VSS 123

RESULT 14  
PL0086  
Ig heavy chain V region (E4) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 23-Jul-1999  
C;Accession: PL0086  
R;Week, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1989  
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A;Reference number: PL0080; MUID:89094248; PMID:2492056  
A;Accession: PL0086  
A;Molecule type: mRNA  
A;Residues: 1-119 <MEE>  
A;Cross-references: UNIPARC:UPI000115F1F; GB:X58595; GB:Y00794; NID:951561; PIDN:CAA414  
A;Experimental source: strain BALB/c  
A;Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal ant  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
Query Match 34.6%; Score 482; DB 2; Length 119;  
Best Local Similarity 75.6%; Pred. No. 2.1e-28;  
Matches 90; Conservative 8; Mismatches 19; Indels 2; Gaps 1;  
QY 3 QVQLQSGAELVRPGTSVKISCKASGYTFNFWLGVKQRPGLGLEWIGDIYPGGGYTN 62  
Db 1 QVQLQSGAELVRPGTSVKISCKASGYTFNFWLGVKQRPGLGLEWIGDIYPGGGYTN 60  
QY 63 NEKFKGKATVTADTSSRTAVQVRSITSEDSAVYFCAR--SASWYFDVWGARTT 119  
Db 61 TORFKAKATLTADKSSSTAYMQLSSLTSDSASVYFCARDDGSGWYFDVWGARTT 119

RESULT 15  
B28195  
Ig kappa chain V region (anti-haloperidol antibody B) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 21-Jan-2000  
C;Accession: B28195  
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.  
J. Biol. Chem. 263, 4059-4063, 1988  
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s  
A;Reference number: A28195; MUID:88153717; PMID:3267217  
A;Accession: B28195  
A;Molecule type: mRNA  
A;Residues: 1-107 <SHE>  
A;Cross-references: UNIPARC:UPI0000114D6A; EMBL:M19767; NID:9197041; PIDN:AAA38892.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>  
Query Match 34.4%; Score 480; DB 2; Length 107;  
Best Local Similarity 86.0%; Pred. No. 2.6e-28;  
Matches 92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
QY 129 DIELTQSPKFMSTSVGDRVSVTKASQNVGNVAMHQQKPGQSPKALIYSASRYSGVPD 188

Db 1 DILMTQSQKFMSTSVGDRVSVTKASQNVGNVAMHQQKPGQSPKALIYSASRYSGVPD 60  
QY 189 RFTGSGSGTDFTLTITISNVQSEDLAEYFCQYHTYPLTFGGGTLEIK 235  
Db 61 RFTGSGSGTDFTLTITNVQSEDLAEYFCQYHTYPLTFGGGTLEIK 107  
Search completed: February 9, 2006, 03:34:18  
Job time : 26.4654 secs

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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:18:36 ; Search time 161.118 Seconds  
(without alignments)  
1147.288 Million cell updates/sec

Title: US-10-049-404-2  
Perfect score: 1395  
Sequence: 1 MAQVQLQSGAEIVRPQTSV.....GSRQKLISEDLNHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	783.5	56.2	243	2	Q7QM2_MOUSE	Q7lqm2 mus musculus
2	725.5	52.0	255	2	Q6KB05_MOUSE	Q6kb05 mus musculus
3	724	51.9	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
4	708	50.8	487	2	Q65ZL2_MOUSE	Q65zl2 mus sp. fv/
5	669	48.0	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
6	630	45.2	241	2	Q921A6_MOUSE	Q921a6 mus musculus
7	584.5	41.9	248	2	Q65ZQ7_MOUSE	Q65zq7 mus sp. b3(
8	527	37.8	168	2	Q8VDC9_MOUSE	Q8vdc9 mus musculus
9	520	37.3	468	2	Q569W9_MOUSE	Q569w9 mus musculus
10	516	37.0	121	1	HV01_MOUSE	P01745 mus musculus
11	515.5	37.0	218	2	Q925S1_MOUSE	Q925s1 mus musculus
12	514.5	36.9	613	2	Q8VCX7_MOUSE	Q8vcx7 mus musculus
13	494	35.4	108	2	Q8VIJ0_MOUSE	Q8vij0 mus musculus
14	491.5	35.2	143	2	Q91V67_MOUSE	Q91v67 mus musculus
15	483	34.6	238	2	Q58E04_MOUSE	Q58e04 mus musculus
16	479	34.3	473	2	Q9D8L4_MOUSE	Q9d8l4 mus musculus
17	472	33.8	120	1	HV03_MOUSE	P01747 mus musculus
18	470.5	33.7	143	2	Q924Q0_MOUSE	Q924q0 mus musculus
19	467.5	33.5	145	2	Q924R3_MOUSE	Q924r3 mus musculus
20	464.5	33.3	463	2	Q99LC4_MOUSE	Q99lc4 mus musculus
21	464	33.3	117	1	HV12_MOUSE	P01756 mus musculus
22	464	33.3	144	2	Q924P5_MOUSE	Q924p5 mus musculus
23	464	33.3	458	2	Q5BJZ2_RAT	Q5bjz2 rattus norv
24	463	33.2	117	1	HV13_MOUSE	P01757 mus musculus
25	462	33.1	149	1	KV5A_MOUSE	P01633 mus musculus
26	462	33.1	486	2	Q8HYZ6_MOUSE	Q8hyz6 mus musculus
27	460.5	33.0	481	2	Q91WT1_MOUSE	Q91wt1 mus musculus
28	459.5	32.9	483	2	Q52L51_MOUSE	Q52l51 mus musculus
29	459	32.9	140	1	HV02_MOUSE	P01746 mus musculus
30	457	32.8	470	2	Q7TMK1_MOUSE	Q7tmk1 mus musculus
31	454.5	32.6	143	2	Q924P9_MOUSE	Q924p9 mus musculus

RESULT 1

ID	Q7QM2_MOUSE PRELIMINARY;	PRT;	243 AA.
AC	Q7QM2;		
DT	01-OCT-2003 (Tremblrel. 25, Created)		
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	ScFv 6H8 protein (Fragment).		
GN	Name=scFv 6H8;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=Balb/C;		
RX	MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;		
RA	Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;		
RA	"scFv single chain antibody variable fragment as inverse agonist for		
RT	the beta-2 adrenergic receptor."		
RL	J. Biol. Chem. 278:36740-36747(2003).		
RL	EMBL; AJ574851; CAB00495.1; -; Genomic_DNA.		
DR	HSSP; P01751; 1A6W.		
DR	SMR; Q7QM2; 1-236.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	SMART; SM00406; IGV; 2.		
DR	PROSITE; PS50835; IG-LIKE; 2.		
FT	NON TER 1		
SQ	SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;		
Query Match 56.2%; Score 783.5; DB 2; Length 243;			
Best Local Similarity 57.5%; Pred. No. 5.4e-56;			
Matches 153; Conservative 34; Mismatches 50; Indels 29; Gaps 4;			
Qy	3	QVQLQSGAEIVRPQTGSKASGYTFYTWLGNWQKRPCHGLIEWIGDIPYGGYTNV	62
Db	1	QVQLQSGSELVRFCASVKLSCKASGYFTTYWVHWYKQKHGQGLEWIGNIPGSGITNY	60
Qy	63	NEKFKGATVTADTSSRTAYVQVRSLSLTSDESAVYFCARSAWYFDVWGARTVTVSSAKT	122
Db	61	DEKFNKGILLTVDTSSTAYVHLSLASEDSAVYVCARGRG-LDVWGAGITLTIVSSGG	119
Qy	123	TPKLGG-----DIELTQSPKFMSTSVCDRVNVTYKASQNVGTNVWQKPGQSPKVL	176
Db	120	GSGGGGGGGSDIQMTQSSSSFSVSLDGRVTITCKASEDINRLAWYQKPGNAPRLLI	179
Qy	177	YSASVRYGVDPRTFTGSGSGDTFTLTISNVOSEDLAIFYCOQHYTYPLTFGGGTKLEIKR	236
Db	180	SGATSLRTGVSPRFGSGSGKDYLTLSLTQEDVATYCCQYWS-TRTFGGGTKLEIK-	237
Qy	237	ADAAAAGSEQKLISEDLNHHHHH 262	

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Db 238 -----HHHHH 243

RESULT 2
Q6KB05 MOUSE
ID Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; A746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 52.0%; Score 725.5; DB 2; Length 255;
Best Local Similarity 52.2%; Pred. No. 3.2e-51;
Matches 144; Conservative 37; Mismatches 58; Indels 37; Gaps 4;

QY 3 QVQLQSGAEIVRPGETSVKISKASGYFTNTYWLGVKQRPGLHLEWIGDIYPGGGYTNV 62
Db 1 QVQLQSGGDLVPGGSLKVCASGFTTSSYGMKSWRQTPDKRLHVAITISGGSYTY 60

QY 63 NEKFKGKATVADTSSRTAYVQVRSITSDSAVYFCAASW----YFDVWGARTTIVTS 118
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYCARHINRYDGAFDYWGQGTTLTVS 120

QY 119 SAKTTPKLG-----DIETQSPKFMSTSVGDRVNTYKASQ-----NVGTNVAWFOQ 166
Db 121 SGGGSGGGGGGGSDIVMAQSPSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQ 180

QY 167 KPQSGPKVLIYSARYSGVDPDFTGSGGTDTFTLTISNVQSEDLAIEYFCQYHYTPTLF 226
Db 181 KPQSGPKLIYGHASTRESGVDPDFTGSGGTDTFTLTISNVQSEDLAIEYFCQYHYTPTLF 240

QY 227 GGGTKLEIKRAAAAAAGSEQKLISEEDLNSHHHHH 262
Db 241 GAGTKLEIK-----HHHHH 255

RESULT 3
Q65ZC8 HUMAN
ID Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q65ZC8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

Db 238 -----HHHHH 243

RESULT 2
Q6KB05 MOUSE
ID Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; A746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 51.9%; Score 724; DB 2; Length 244;
Best Local Similarity 57.4%; Pred. No. 4e-51;
Matches 140; Conservative 39; Mismatches 55; Indels 10; Gaps 2;

QY 3 QVQLQSGAEIVRPGETSVKISKASGYFTNTYWLGVKQRPGLHLEWIGDIYPGGGYTNV 62
Db 1 QVQLQSGAEIVKPKGDSVKVSKASGYFTSDHYHMHVVRQAPGGLEWGWIDPNNGDTRF 60

QY 63 NEKFKGKATVADTSSRTAYVQVRSITSDSAVYFCAR----SASWYFDVWGARTTIVTS 118
Db 61 AQRFGQGVMTTRDTSISAAYMEVSRILSDDTAVYVCAREGTGSAIYGMVDVWGQGTTLTVS 120

QY 119 SAKTTPKLG-----DIETQSPKFMSTSVGDRVNTYKASQNVGTNVAWFOQKPGQSP 172
Db 121 SGGGSGGGGGGGSDIQMTQSPSTLSASIGDRVITICRASEGIYHVLAWYQQKPGKAP 180

QY 173 KVLIVSASVRYSGVDPDFTGSGGTDTFTLTISNVQSEDLAIEYFCQYHYTPTLF 232
Db 181 KFLIVKASSLASGAPSRFSGSGGTDTFTLTISLQPDPTATYCCQYSNYPLTFFGGGTKL 240

QY 233 EIKR 236
Db 241 EIKR 244

RESULT 4
Q65ZL2 9MURI
ID Q65ZL2_9MURI PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN- $\gamma$ ;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=96272580; PubMed=8688499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -; mRNA.
DR GO; GO:0003823; Fc antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00409; IG; 3.  
DR SMART; SM00407; IGc1; 2.  
DR SMART; SM00408; IGc2; 2.  
DR SMART; SM00406; IGv; 2.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 1.  
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 50.8%; Score 708; DB 2; Length 487;  
Best Local Similarity 56.7%; Pred. No. 1.9e-49;  
Matches 139; Conservative 37; Mismatches 49; Indels 20; Gaps 3;

QY 2 AOVLQOSGAELVRPGTSVKISCKASGYTFNTYWLGNVKQRPQGHLEWICDIYPGGGYTN 61  
DB 19 SQVLQOSDAELVKPGASVKISCKASGYTFDHAHIAHWAKQPKQGLEWIGYISPGNDIK 78  
QY 62 YNEKFKGKATVTADTSSRTAYVQVRLTSDSNAVYFCARSASWYFDVWGARTTTVSSAK 121  
DB 79 YNEKFKGKATLTADKSSSTAYMQLNSLTSDSNAVYFCARS--YYGHWGQGTTLTGSGG- 134  
QY 122 TTPKLG-----IELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQ 170  
DB 135 -----GGSGGGSGGGSGRIQMTQSPASLSVSGELVITTCRASENIYSLNLAWYQOKQK 189  
QY 171 SPKVLVYSARYSGVDPDRFTGSGSGTDTLTISNVQSEDLAIFYCQOYHTYPLTFGGGT 230  
DB 190 SPQLVYATNLADGVPSRFSGGSGGTQYSLKINSQSEDFGSYYCQHFVGTPTTGGGT 249  
QY 231 KLEIK 235  
DB 250 RLEIK 254

RESULT 5  
Q65ZC9 HUMAN  
ID Q65ZC9\_HUMAN PRELIMINARY; PRT; 240 AA.  
AC Q65ZC9\_2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Single-chain Fv (Fragment).  
GN Name=acFv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C1q/7;  
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbr0797-629;  
RA Kontermann R.E., Ming M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies.";  
RL Nat. Biotechnol. 15:629-631(1997).  
DR EMBL; Y13056; CAA73499.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGv; 2.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 240 240  
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 48.0%; Score 669; DB 2; Length 240;  
Best Local Similarity 54.2%; Pred. No. 1.3e-46;  
Matches 130; Conservative 37; Mismatches 67; Indels 6; Gaps 1;

QY 3 QVQLQOSGAELVRPGTSVKISCKASGYTFNTYWLGNVKQRPQGHLEWIGDIYPGGGYTN 62  
DB 1 QVQLVQSGGGLVQPGGSLRISCAASGTFPSYGMHWVRQAPGKLEWVAIVSYDGSNKY 60

QY 63 NEKFKGKATVTADTSSRTAYVQVRLTSDSNAVYFCARSASWYFDVWGARTTTVSSAKT 122  
DB 61 ADSVKGRFTISRDNSKNTLYLQWNSLRADTAIVYCARDWGSGLDLPWGKGTTLTVSSGG 120  
QY 123 TTPKLG-----DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQSPKVL 176  
DB 121 GSGGGSGGGSGDIQMTQSPSTLSASIGDRVITTCRASGIYRWLAWYQOKPGKAPKLLI 180  
QY 177 YSASVRYSGVDPDRFTGSGSGTDTLTISNVQSEDLAIFYCQOYHTYPLTFGGGTLEIKR 236  
DB 181 YKASSLASRAPSRFSGSGSGTDTLTISLQPDPAFYICQYSNYPLTFGGGTLEIKR 240  
RESULT 6  
Q921A6 MOUSE  
ID Q921A6\_MOUSE PRELIMINARY; PRT; 241 AA.  
AC Q921A6\_2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 26, Last annotation update)  
DE Anti-CEA 79 single chain Fv (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98170165; PubMed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scFv).";  
RL Mol. Cells 7:816-819(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;  
RA Stark S.E., Caton A.J.;  
RT "Antibodies that are specific for a single amino acid interchange in a  
RT protein epitope use structurally distinct variable regions.";  
RL J. Exp. Med. 174:613-624(1991).  
DR EMBL; U88067; AAB48044.1; -; mRNA.  
DR PIR; S19965; S19965.  
DR PIR; S19967; S19967.  
DR PIR; S19968; S19968.  
DR PIR; S26325; S26325.  
DR HSSP; P01607; 1BWV.  
DR Ensembl; ENSMUSG0000021155; Mus musculus.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IG; 2.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 241 241  
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 45.2%; Score 630; DB 2; Length 241;  
Best Local Similarity 52.1%; Pred. No. 2e-43;  
Matches 126; Conservative 37; Mismatches 71; Indels 8; Gaps 3;

QY 3 QVQLQOSGAELVRPGTSVKISCKASGYTFNTYWLGNVKQRPQGHLEWIGDIYPGGGYTN 62  
DB 1 QVQLQOSGPELKKPGETVKISCKASGYTFDYGNWVWQAPGKLGWGWINTVYTGPTY 60  
QY 63 NEKFKGKATVTADTSSRTAYVQVRLTSDSNAVYFCAR-SASWYFDVWGARTTTVSSAK 121  
DB 61 ADFFKGRFAPSLFSTASTAYLQINLNKEDTAYFCARDLLRYFDYWGQGTTLTVSSGG 120  
QY 122 TTPKLG-----DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQSPKVL 175  
DB 121 GSGGGSGGGSGDIELTQSPSSLASLGKGVITTCASQDINKYIAWYQHKPGKPRSA 180

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QY 176 IYSASRYGVDRFTGSGSGDTFTLTISNVOSEDLAIFYCOQHYHYPLTFGGTKLEIK 235
Db 181 HTLHYIQGIPSRFSGSGGRDYSFSISNLNLPEDATYYCLHYDNLH-TFGGTKLEIK 239
QY 236 RA 237
Db 240 RA 241

RESULT 7
ID Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE B3 (Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=BALE/c;
RA Sembi P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=BALE/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ416332; CAC94867.1; -; mRNA.
DR HSP; P01863; IE4W.
DR SMR; QBVDC9; 20-168.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 168
SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;

Query Match 37.8%; Score 527; DB 2; Length 168;
Best Local Similarity 78.2%; Pred. No. 3 5e-35;
Matches 97; Conservative 11; Mismatches 14; Indels 2; Gaps 1;

QY 2 AQVOLQSGAELVRPGTSVKISCKASGYFTTNYLWGWKQRPQGHLEWIGDIYPGGYTN 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 SQVOLQSGAELMKPGASVKISKATGYTFSSYWDWVKQRPQGHLEWIGILPGSGRTN 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 YNEKFGKATVTADTSSRTAYVQVSLTSEDSAVYFCAR--SASWYEDVGARTTTVSS 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 YNEKFGKATVTADTSSRTAYVQVSLTSEDSAVYFCAR--SASWYEDVGARTTTVSS 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 AKTT 123
Db 139 TKTT 142

RESULT 9
Q569W9 MOUSE
ID Q569W9_MOUSE PRELIMINARY; PRT; 468 AA.
AC Q569W9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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QY 176 IYSASRYGVDRFTGSGSGDTFTLTISNVOSEDLAIFYCOQHYHYPLTFGGTKLEIK 235
Db 181 HTLHYIQGIPSRFSGSGGRDYSFSISNLNLPEDATYYCLHYDNLH-TFGGTKLEIK 239
QY 236 RA 237
Db 240 RA 241

RESULT 7
ID Q65ZQ7_9MURI PRELIMINARY; PRT; 248 AA.
AC Q65ZQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE B3 (Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=BALE/c;
RA Sembi P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=BALE/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ416332; CAC94867.1; -; mRNA.
DR HSP; P01863; IE4W.
DR SMR; QBVDC9; 20-168.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43B570950 CRC64;

Query Match 41.9%; Score 584.5; DB 2; Length 248;
Best Local Similarity 47.8%; Pred. No. 1.1e-39;
Matches 117; Conservative 42; Mismatches 73; Indels 13; Gaps 3;

QY 4 VOLQSGAELVRPGTSVKISCKASGYFTTNYLWGWKQRPQGHLEWIGDIYPGGYTN 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 VKLVSGGGLVQPGSLKLSKATSGFTFSDYMYWVQTPKRLWVAYISNDSSAAYS 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 EKPFKGRATVTADTSSRTAYVQVSLTSEDSAVYFCARSASW--YFDVWGARTTTVTSSAK 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 DTVKGRFTISRDNARNTLYIQMSRLKSEDTAIYSCARGLAAGWAFAYWGQTLVTVSSGG 122
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 TTPKLG-----DIELTQSPKFMSTSVGDRVNVTVKASQ-----NVGTVNAWFOQKPGQ 170
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 GSGSGGGGGGGSDVLMTQSLPVLSDQASISCRSQIIVHSGNTYLEYLOKPGQ 182
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 171 SPKVLIVASRYSGVDPDFTGSGSGTDTFTLTISNVQSEDLAIFYCOQHYHYPLTFGGT 230
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 SPKLLIVKNSRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVIYCFQGSHPFTFGSGT 242
|||||
QY 231 KLEIK 235
Db 243 KLEIK 247

RESULT 8
Q8VDC9 MOUSE
ID Q8VDC9_MOUSE PRELIMINARY; PRT; 168 AA.
AC Q8VDC9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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RL World J. Gastroenterol. 6:709-717(2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BALB/c;  
RA Cui D., Zeng G., Yan X., Li X., Su C.;  
RT "Cloning of mouse genes related to repairing of intestinal epithelium  
of the irradiated mice by treatment with the intestinal RNA of mice of  
the same strain."  
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
DR EMBL; AF240168; AAK43733.1; -; mRNA.  
DR HSP; P01665; IONZ.  
DR Ensembl; ENSMUSG0000058040; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 218 218  
SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;  
  
Query Match 37.0%; Score 515.5; DB 2; Length 218;  
Best Local Similarity 50.7%; Pred. No. 4.2e-34;  
Matches 110; Conservative 33; Mismatches 57; Indels 17; Gaps 5;  
  
QY 1 MAQVQLQDSGAELVRPGTGVKISKASGYTFNVLGWKQRPCHGLEWIGDIPGGYV 60  
Db 1 MAQVQLQDSGAELVRPGTGVKISKASGYTFNVLGWKQRPCHGLEWIGDIPGGYV 60  
  
QY 61 NYNEKFKGKATVTADTSSTRTAYVQVRSLSSEDSAVYFCARSASWYFD ---VMGARTT 116  
Db 61 NYNEKFKGKATVTADTSSTRTAYVQVRSLSSEDSAVYFCARSASWYFD ---VMGARTT 116  
  
QY 117 VSSAKTTPKLG-----DIETQSPKFMSTVGDVRNVTYKASQ---NVGN-VAWFOQ 166  
Db 117 VSSAKTTPKLG-----DIETQSPKFMSTVGDVRNVTYKASQ---NVGN-VAWFOQ 166  
  
QY 167 KQSQSKVLIVSYASYSGVDPDFTGSGSGTDFTLI 203  
Db 178 KPGQPKLLIYAASQKQSGVPGAGLLASGSGTDFSLNI 214  
  
RESULT 12  
Q8VCX7\_MOUSE PRELIMINARY; PRT; 613 AA.  
AC Q8VCX7;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Igh-6 protein.  
GN Name=Igh-6;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
RA Klauniger R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2464031;  
RA Sikder S.K., Borden P., Gruezo F., Alolkar P.N., Bhattacharya S.B.,  
RA Morrison S.L., Kabat E.A.;  
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the  
antigen-binding of monoclonal antibodies to alpha(1---6)dextran."  
RL J. Immunol. 142:888-893(1989).  
DR EMBL; BC018315; AAH18315.1; -; mRNA.  
DR FIR; C30562; C30562.  
DR HSP; P01751; LA6W.  
DR Ensembl; ENSMUSG0000054328; Mus musculus.  
DR MGI; MGI:96448; Igh-6.  
DR GO; GO:0019815; C:B cell receptor complex; IDA.  
DR GO; GO:0003897; C:external side of plasma membrane; IDA.  
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
DR GO; GO:0048471; C:perinuclear region; IDA.  
DR GO; GO:0003823; F:antigen binding; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
DR GO; GO:0000187; P:activation of MAPK activity; IDA.  
DR GO; GO:0003033; P:antigen processing; IDA.  
DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.  
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.  
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.  
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.  
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . .; IDA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;  
  
Query Match 36.9%; Score 514.5; DB 2; Length 613;  
Best Local Similarity 79.8%; Pred. No. 1.8e-33;  
Matches 95; Conservative 11; Mismatches 12; Indels 1; Gaps 1;  
  
QY 2 AQVQLQDSGAELVRPGTGVKISKASGYTFNVLGWKQRPCHGLEWIGDIPGGYV 61  
Db 19 SQVQLQDSGAELVRPGTGVKISKATGYTFSSWVWVQRPCHGLEWIGDIPGGYV 78  
  
QY 62 YNEKFKGKATVTADTSSTRTAYVQVRSLSSEDSAVYFCARS-ASWYFDVWGARTT 119  
Db 79 YNEKFKGKATVTADTSSTRTAYVQVRSLSSEDSAVYFCARRLGRWYFDVWGARTT 137  
  
RESULT 13  
Q8VJ0\_MOUSE PRELIMINARY; PRT; 108 AA.  
AC Q8VJ0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-DNA light chain (Fragment).  
GN Name=Igh-V19-14; Synonyms=Vk19;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/HeJ-lpr/lpr;
RA MEDLINE=96409289; PubMed=8814271;
RX Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=2499887;
RX Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RA "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RX Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RA "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW)F1 mice.";
RL J. Exp. Med. 176:761-779(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91115823; PubMed=1703527;
RX Goshorn S.C., Retzel E., Jemerson R.;
RA "Common structural features among monoclonal antibodies binding the
RT same antigenic region of cytochrome c.";
RL J. Biol. Chem. 266:2134-2142(1991).
DR EMBL; U59155; AAB02917.1; -; mRNA.
DR PIR; A33933; A33933.
DR PIR; A37262; A37262.
DR PIR; PH1072; PH1072.
DR HSSP; P01634; 11GC.
DR SMR; Q8VIJ0; 1-108.
DR Ensembl; ENSMUSG0000053690; Mus musculus.
DR MGI; MGI:1330830; Igk-V19-14.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFEE CRC64;

Query Match 35.4%; Score 494; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 1e-32; Indels 0; Gaps 0;
Matches 95; Conservative 5; Mismatches 8;

QY 129 DIELTOSPKFMTSVGDRVNVTKASQNVGTNVAVFQKPGQSPKVLIIYSASYRSGVPD 188
DB 1 DIVMTQSQTFTSVISGDRSVTKASQNVGTNVAVYQKPGQSPKALIIYSASYPSYGVPH 60

QY 189 RFTGSGSGTDTLTISNVQSEDIAEYFCQYHYPLTFGGGKLEIKR 236
DB 61 RFTGSGSGTDTLTISNVQSEDIAEYFCQYNSYPYTFGGGKLEIKR 108

RESULT 14
Q91V67 MOUSE
ID Q91V67 MOUSE PRELIMINARY; PRT; 143 AA.
AC Q91V67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN Name=VH186.2-D-J-C mu; Synonym=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB069912; BAB63928.1; -; mRNA.
DR EMBL; AB069914; BAB63930.1; -; mRNA.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1AGW.
DR SMR; Q91V67; 1-129.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
FT NON_TER 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

Query Match 35.2%; Score 491.5; DB 2; Length 143;
Best Local Similarity 78.0%; Pred. No. 2.3e-32;
Matches 92; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 3 QVQLQSGAELVRPGTTSVKISKASGYTFTNTWLGWVKQRPQGHLEWIGDIYVPGGYTNY 62
DB 1 QVQLQPGAELVRPGTTSVKLSCKASGYTFTSYMMHWVKQRPQGLEWIGVIDPSDYTY 60

QY 63 NKKPKGKATVADTSSRTAYQVRSLSYTSVDSAVYFCARSA-SWYFDWGARTTTVTSS 119
DB 61 NQKFKGKATLTVDTSSTAYMQLSSLTSDSAVYCAPTYVDWDFVWVGTTTVTSS 118

RESULT 15
Q58EU4 MOUSE
ID Q58EU4 MOUSE PRELIMINARY; PRT; 238 AA.
AC Q58EU4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091754; AAH91754.1; -; mRNA.
DR SMR; Q58EU4; 25-238.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 238 AA; 26440 MW; AE2B2BA90B9F7D5D CRC64;

Query Match      34.6%; Score 483; DB 2; Length 238;
Best Local Similarity 82.3%; Pred. No. 2.1e-31;
Matches 93; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 128 GDIELTQSPKEWSTSYGDRVNVYKASQNVGTNVAVFQOKPGQSPKVLISASRYSGYP 187
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   24 GDIVMTQSHKFMSTSGDRVSIICKASQDVTTAVAWYQOKPGQSPKVLHWASTRHTGVP 83

Qy 188 DRFTGSGSGTDFLTITISNVQSEDLAEYFCQQYHTYPLTFGGGTKLEIKRADAA 240
Db   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   84 DRFTGSGSGTDFLTITISNVQSEDLADYFCQQYSSYPLTFGSGTKLEIKRADAA 136

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Search completed: February 9, 2006, 03:33:22  
Job time : 165.118 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 9, 2006, 03:33:41 ; Search time 34.7701 Seconds  
(without alignments)  
622.979 Million cell updates/sec

Title: US-10-049-404-2  
Perfect score: 1395  
Sequence: 1 MAQVQLQSGAELVRPCTSV.....GSEQLISEDLNHHHHH 262

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5 COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTRUS COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867.5	62.2	288	2	US-09-423-439-38
2	862.5	61.8	249	1	US-08-797-689-18
3	862.5	61.8	249	2	US-09-984-186-18
4	858	61.5	240	2	US-10-096-246A-35
5	856	61.4	240	2	US-10-092-246-36
6	856	61.4	240	2	US-10-096-246A-37
7	853	61.1	240	2	US-10-092-246-35
8	848	60.8	240	2	US-10-096-246A-36
9	841	60.3	240	2	US-10-092-246-37
10	819.5	58.7	239	2	US-10-092-246-33
11	819.5	58.7	239	2	US-10-096-246A-33
12	814.5	58.4	257	2	US-10-092-246-2
13	814.5	58.4	257	2	US-10-096-246A-2
14	813	58.3	240	2	US-10-096-246A-34
15	811	58.1	264	2	US-10-114-716A-46
16	808	57.9	240	2	US-10-092-246-34
17	804.5	57.7	239	2	US-10-092-246-32
18	804.5	57.7	239	2	US-10-096-246A-32
19	798.5	57.2	246	1	US-08-469-486-57
20	798.5	57.2	246	1	US-08-469-658-57
21	786.5	56.4	673	2	US-09-423-439-37
22	783.5	56.2	355	2	US-08-875-811-57
23	779	55.8	269	2	US-08-646-265A-109
24	774	55.5	258	2	US-09-526-738A-4
25	766	54.9	273	1	US-08-403-853-18
26	765.5	54.9	250	1	US-08-133-804-2
27	765.5	54.9	250	1	US-08-461-184-8

28	765.5	54.9	250	1	US-08-463-675-8	Sequence 8, Appli
29	765.5	54.9	250	1	US-08-464-589-8	Sequence 8, Appli
30	765.5	54.9	250	1	US-08-461-838-2	Sequence 2, Appli
31	765.5	54.9	250	1	US-08-461-386-2	Sequence 2, Appli
32	765	54.8	256	2	US-09-526-738A-2	Sequence 10, Appl
33	764	54.8	271	1	US-08-894-922A-10	Sequence 30, Appl
34	760.5	54.5	267	2	US-09-419-788-30	Sequence 22, Appl
35	760	54.5	288	2	US-09-818-247-22	Sequence 16, Appl
36	759.5	54.4	553	1	US-08-661-052-16	Sequence 16, Appl
37	759.5	54.4	553	2	US-09-188-082-16	Sequence 16, Appl
38	759.5	54.4	553	2	US-09-364-088-16	Sequence 16, Appl
39	759.5	54.4	553	2	US-09-102-716-16	Sequence 19, Appl
40	758.5	54.4	483	1	US-08-392-338A-19	Sequence 19, Appl
41	758.5	54.4	483	2	US-09-166-750-19	Sequence 19, Appl
42	758.5	54.4	483	2	US-09-166-093-19	Sequence 19, Appl
43	758.5	54.4	483	2	US-09-172-019-19	Sequence 19, Appl
44	758.5	54.4	483	2	US-09-166-094-19	Sequence 19, Appl
45	758.5	54.4	483	2	US-09-443-213-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-09-423-439-38  
; Sequence 38, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423,439  
; FILING DATE: 09-No. 6339070-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-423-439-38

Query Match	62.2%	Score	867.5	DB 2	Length	288			
Best Local Similarity	62.8%	Pred. No.	5.7e-63						
Matches	174	Conservative	35	Mismatches	43	Indels	25	Gaps	5
Qy	1	MAQVQLQSGAELVRPCTSVKISKASGYTFTNWLGVKORPGHLEWIGDIYVGGGYT	60						
Db	21	MAQVQLQPGNELVKPGASVQLSCASGYITGTGWIHWKORPGGLEWIGVNPSTGRS	80						
Qy	61	NYNEKFKGKATVTADTSRTAYQVRSITSDESAVYFCARSASWYF----	DWGARTT	116					





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QY 1 MAQVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWVKQRPQGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSDSAVYFCARSASWYFDVWGARTTTVSSA 120
DB 61 NYSETFKGKATLTVDTSSTNTVMQLSSLTSEDVAVFCARGVG--LDYWGQGTITVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSGDVRVNTYTKASQNVGNTNVAWFQOKPGQSPKV 174
DB 119 GGGSGGGGGGGSDIELTQSPNSLSTSGDRIKITCKASQVDVTAAGWYQORPGQSPKL 178
QY 175 LIYSASYRVSGVDPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQOYHTYPLTFGGGTKLEI 234
DB 179 LIFWSSTRHTGVDPDRFTGSGSGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLEI 238
QY 235 KR 236
DB 239 KR 240
```

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RESULT 7
US-10-092-246-35
; Sequence 35, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-35
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Query Match 61.1%; Score 853; DB 2; Length 240;
Best Local Similarity 68.6%; Pred. No. 6.9e-62;
Matches 166; Conservative 25; Mismatches 43; Indels 8; Gaps 2;

QY 1 MAQVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWVKQRPQGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSDSAVYFCARSASWYFDVWGARTTTVSSA 120
DB 61 NYSETFKGKATLTVDTSSTNTVMQLSSLTSEDVAVFCARGVG--LDYWGQGTITVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSGDVRVNTYTKASQNVGNTNVAWFQOKPGQSPKV 174
DB 119 GGGSGGGGGGGSDIELTQSPKVVTSIGDRIKITCKASQVDVTAAGWYQORPGQSPKL 178
QY 175 LIYSASYRVSGVDPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQOYHTYPLTFGGGTKLEI 234
DB 179 LIFWSSTRHTGVDPDRFTGSGSGTDFTLTISNAQSEDLADYFCHQYSSHPFTFGSGTKLEI 238
QY 235 KR 236
DB 239 KR 240
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RESULT 8
US-10-096-246A-36
; Sequence 36, Application US/10096246A
; Patent No. 6818748
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; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal scFv Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-36
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Query Match 60.8%; Score 848; DB 2; Length 240;
Best Local Similarity 68.6%; Pred. No. 1.8e-61;
Matches 166; Conservative 24; Mismatches 44; Indels 8; Gaps 2;

QY 1 MAQVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWVKQRPQGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKSGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
QY 61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSDSAVYFCARSASWYFDVWGARTTTVSSA 120
DB 61 NYSETFKGKATLTVDTSSTNTVMQLSSLTSEDVAVFCARGVG--LDYWGQGTITVTVSSG 118
QY 121 KTTPKLGG-----DIELTQSPKFMSTSGDVRVNTYTKASQNVGNTNVAWFQOKPGQSPKV 174
DB 119 GGGSGGGGGGGSDIELTQSPNSLSTSIGDRIKITCKASQVDVTAAGWYQORPGQSPKL 178
QY 175 LIYSASYRVSGVDPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQOYHTYPLTFGGGTKLEI 234
DB 179 LIFWSSTRHTGVDPDRFTGSGSGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLEI 238
QY 235 KR 236
DB 239 KR 240
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RESULT 9
US-10-092-246-37
; Sequence 37, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of M
; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-37
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Query Match 60.3%; Score 841; DB 2; Length 240;
Best Local Similarity 68.2%; Pred. No. 6.6e-61;
Matches 165; Conservative 24; Mismatches 45; Indels 8; Gaps 2;

QY 1 MAQVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWVKQRPQGHGLEWIGDIYPGGGYT 60
DB 1 MAQVQLQESGPELVKPGASVKISKASGYTFTDYHVVHWKRGKPGQGLEWIGMTYPGFDNT 60
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Qy

63

NEKPKGKATVTADTSSTAYQVRSLSSEDSAVYFCARSASWYFDVWGARTTIVTS

AKT

122

Db

61

NQKPKSATLTVDKSSSTAYMELHSLTSEDSAVYFCARFSS--FDYWGQGT

TTVTVSSG--

116

Qy

123

TPKLGG-----DIELTQSPKFMSTSVGDRVNVITYKASONVGTNVAWFQ

QKPGQ

170

Db

117

---GGGGGVGGGGGSDIQMTQSPSSLASLGDITITICHASONINWLSWYQ

KPGN

172

Qy

171

SPKVLIIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEVFCQO

VHTYPLTFGGGT

230

Db

173

IPKLLIYRASNLHTGVPSRFGSGSGTGFTLTISLQPEDIAITYCQGGQ

SYPLTFGTGT

232

Qy

231

KLEIKRADA----AAAGSEQKLISEEDLN

255

Db

233

KLEIKRAAAHHHHHHHGAEGKLISEEDLN

261

Search completed: February 9, 2006, 03:35:34

Job time : 35.7701 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 03:53:23 ; Search time 122.43 Seconds  
(without alignments)  
894.155 Million cell updates/sec

Title: US-10-049-404-2  
 Perfect score: 1395  
 Sequence: 1 MAOVLQOOSGAEIVRPGTSV.....GSEQKLISEEDLNSHHHHH 262

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 1867569

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications AA Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.rep:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.rep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.rep:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	895.5	64.2	240	5	US-10-482-630-51	Sequence 51, Appl
2	891.5	63.9	296	5	US-10-784-305-2	Sequence 2, Appl
3	862.5	61.8	249	3	US-09-984-186-18	Sequence 18, Appl
4	862.5	61.8	249	4	US-10-237-667-18	Sequence 18, Appl
5	862.5	61.8	249	4	US-10-237-708-18	Sequence 18, Appl
6	862.5	61.8	249	4	US-10-237-866-18	Sequence 18, Appl
7	862.5	61.8	249	4	US-10-237-871-18	Sequence 18, Appl
8	862.5	61.8	249	4	US-10-237-624-18	Sequence 18, Appl
9	862.5	61.8	249	4	US-10-702-536-18	Sequence 18, Appl
10	862.5	61.8	249	4	US-10-702-636-18	Sequence 18, Appl
11	862.5	61.8	249	6	US-11-146-077-18	Sequence 2, Appl
12	862.5	61.8	622	4	US-10-378-832A-2	Sequence 2, Appl
13	856.5	61.4	255	5	US-10-511-794-21	Sequence 21, Appl
14	856	61.4	240	4	US-10-096-246-36	Sequence 36, Appl
15	853	61.1	240	4	US-10-096-246-35	Sequence 35, Appl
16	847.5	60.8	243	5	US-10-879-994-10	Sequence 10, Appl
17	847.5	60.8	243	5	US-10-610-452-10	Sequence 10, Appl
18	846	60.6	258	4	US-10-239-656-59	Sequence 59, Appl
19	842.5	60.4	291	6	US-11-093-103-102	Sequence 102, Appl
20	841	60.3	240	4	US-10-096-246-37	Sequence 37, Appl
21	839.5	59.5	331	4	US-10-059-261-169	Sequence 169, Appl
22	839.5	59.5	331	5	US-10-627-649-169	Sequence 169, Appl
23	819.5	58.7	239	4	US-10-096-246-33	Sequence 33, Appl
24	814.5	58.4	257	4	US-10-096-246-2	Sequence 2, Appl
25	811	58.1	264	4	US-10-114-176A-46	Sequence 46, Appl
26	811	58.1	264	5	US-10-930-548-46	Sequence 46, Appl
27	808	57.9	240	4	US-10-096-246-34	Sequence 34, Appl

## ALIGNMENTS

## RESULT 1

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US-10-482-630-51
; Sequence 51, Application US/10482630
; Publication No: US20040242851a1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Antibodies That
; FILE REFERENCE: 11245/48502
; CURRENT APPLICATION NUMBER: US/10/482,630
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/US02/20332
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/301,299
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 51
; LENGTH: 240
; TYPE: prt
; ORGANISM: Mouse
; US-10-482-630-51

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[illegible]

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; Publication No. US20050118569A1
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie P.
; APPLICANT: Alvi, Azhar Z.
; APPLICANT: Hu, Wei-Gang
; TITLE OF INVENTION: Genetic Engineering of Streptavidin-Binding Peptide Tagged
; TITLE OF INVENTION: Single-Chain Variable Fragment Antibody to Venezuelan Equine
; FILE REFERENCE: NEL-0018
; CURRENT APPLICATION NUMBER: US/10/784,305
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: 60/448,902
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: scpv: 1-269;
; OTHER INFORMATION: SBP,6His and spacers: 270-296
US-10-784-305-2

Query Match 63.9%; Score 891.5; DB 5; Length 296;
Best Local Similarity 64.8%; Pred. No. 8.7e-60;
Matches 177; Conservative 26; Mismatches 57; Indels 13; Gaps 3;

QY 1 MAQVQLQSGAEIVRGTSVKISKASGYFTNYWLGWVKQRPQGHLEWIGDIYPGGYT 60
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 26 MAQVQLQSGPELVKPGASVKISKASGYFTDYHVHVWVKRPGQGLEWIGMTPGFDNT 85
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 NYNEKFGKATVTADTSSRTAYVQVRSITSEDSAVYFCARSASWYFDVNGARTTVSSA 120
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 86 NYSETFGKATLVDTSSNTVYVQVRSITSEDSAVYFCARGVG--LDYWGQGTITVSSG 143
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 KTTPTKLG-----DIETQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQOKPGQSPKV 174
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 144 GGGSGGGGGGGSDIELTQSPNSLSTSGDRIRITCKASQVDVDTAVGWYQRPQSPKL 203
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 175 LIYSARYRSGVDPDRFTGSGSGTDTLTISNVQSEDLAEYFCQYHTYPLTFTGGGKLEI 234
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 204 LIFWSSTRHTGTVPDRFTGSGSGTDTLTISNVQSEDLADYFCHQYSSYPTFTGSGTKLEI 263
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 235 KRADAAAGS-----EQKLISEEDLNSHHHHH 262
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 264 KRAAHSGGGGPGCHPQPPRCYAGGGGSHHHHH 296
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 3
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. US2002015101A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
;
; Publication No. US20030022308A1
; Sequence 18, Application US/10237667
; Patent No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
;
; Publication No. US20050118569A1
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie P.
; APPLICANT: Alvi, Azhar Z.
; APPLICANT: Hu, Wei-Gang
; TITLE OF INVENTION: Genetic Engineering of Streptavidin-Binding Peptide Tagged
; TITLE OF INVENTION: Single-Chain Variable Fragment Antibody to Venezuelan Equine
; FILE REFERENCE: NEL-0018
; CURRENT APPLICATION NUMBER: US/10/784,305
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: 60/448,902
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: scpv: 1-269;
; OTHER INFORMATION: SBP,6His and spacers: 270-296
US-10-784-305-2
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; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

Query Match 61.8%; Score 862.5; DB 3; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVRGTSVKISKASGYFTNTWLGWVKQRPQGHLEWIGDIYPGGYTNY 62
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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 NEKFKGKATVTADTSSRTAYVQVRSITSEDSAVYFCARSAS-----WYEDVWGARTTV 115
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 64 NKFGKATLVDTSSNTVYVQVRSITSEDSAVYFCAKENRFDERGYAMYWGQGTIV 123
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 116 TVSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNVVTKASQNVGTNVAVFQOKPG 169
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 124 TVSSGGGGGGGGGGSGGSGNIQLTQSPNSMSTSVGDRVSVITCKASQDVDTSVAVYQKPG 183
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QY 170 QSPKVLIIYSARYRSGVDPDRFTGSGSGTDTLTISNVQSEDLAEYFCQYHTYPLTFTGGG 229
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 244 TKLEIK 249
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 4
US-10-237-667-18
; Sequence 18, Application US/10237667
; Publication No. US20030022308A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
;
; Publication No. US20050118569A1
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie P.
; APPLICANT: Alvi, Azhar Z.
; APPLICANT: Hu, Wei-Gang
; TITLE OF INVENTION: Genetic Engineering of Streptavidin-Binding Peptide Tagged
; TITLE OF INVENTION: Single-Chain Variable Fragment Antibody to Venezuelan Equine
; FILE REFERENCE: NEL-0018
; CURRENT APPLICATION NUMBER: US/10/784,305
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: 60/448,902
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: scpv: 1-269;
; OTHER INFORMATION: SBP,6His and spacers: 270-296
US-10-784-305-2
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ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/237,667  
FILING DATE: 10-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-JAN-1997  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-JAN-1992  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-237-667-18  
Query Match 61.8%; Score 862.5; DB 4; Length 249;  
Best Local Similarity 69.5%; Pred. No. 1.2e-57;  
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;  
Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNYWLGWVKQRPCHGLEWIGDIYPGGGYTN 62  
Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNNWVKQRPQGLEWIGRIYPGDGTKY 63  
Qy 63 NEKPKGATVTADTSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYFDVWGARTTV 115  
Db 64 NGKPKGATLTADRSSSTAYWQLSSLTSVGSVAVYFCAKENRPFDERGYANDYWGQGTIV 123  
Qy 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNTYKASQNVGNTVAVFQKPG 169  
Db 124 TVSSGGGGGGGGGGGSGNSQLTQSPNSMSTSVGDRVSIITCKASQDVDTSVAVYQKPG 183  
Qy 170 QSPKVLIVSARYSGVDPDRFTGSGGTDFTLTISNQSEDLAYFCQOYHYTPLTFGGG 229  
Db 184 QSPKLLIYWASTRTGTVPDRFTGSGGTDFTLTISNQSEDSADYFCQOYSSYPWTFTGGG 243  
Qy 230 TKLEIK 235  
Db 244 TKLEIK 249  
RESULT 5  
US-10-237-708-18  
; Sequence 18, Application US/10237708  
; Publication No. US20030036170A1  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; Fournier, Alain  
; Guittou, Jean-Dominique  
; ;  
Jung, Gerard  
Yeh, Patrice  
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
CONTAINING SAID POLYPEPTIDES  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/237,708  
FILING DATE: 10-Sep-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-JAN-1997  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-JAN-1992  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-237-708-18  
Query Match 61.8%; Score 862.5; DB 4; Length 249;  
Best Local Similarity 69.5%; Pred. No. 1.2e-57;  
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;  
Qy 3 QVQLQSGAEIVRPGTSVKISKASGYFTNYWLGWVKQRPCHGLEWIGDIYPGGGYTN 62  
Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNNWVKQRPQGLEWIGRIYPGDGTKY 63  
Qy 63 NEKPKGATVTADTSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYFDVWGARTTV 115  
Db 64 NGKPKGATLTADRSSSTAYWQLSSLTSVGSVAVYFCAKENRPFDERGYANDYWGQGTIV 123  
Qy 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNTYKASQNVGNTVAVFQKPG 169  
Db 124 TVSSGGGGGGGGGGGSGNSQLTQSPNSMSTSVGDRVSIITCKASQDVDTSVAVYQKPG 183  
Qy 170 QSPKVLIVSARYSGVDPDRFTGSGGTDFTLTISNQSEDLAYFCQOYHYTPLTFGGG 229  
Db 184 QSPKLLIYWASTRTGTVPDRFTGSGGTDFTLTISNQSEDSADYFCQOYSSYPWTFTGGG 243  
Qy 230 TKLEIK 235  
Db 244 TKLEIK 249  
RESULT 6  
US-10-237-708-18  
; Sequence 18, Application US/10237708  
; Publication No. US20030036170A1  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; Fournier, Alain  
; Guittou, Jean-Dominique  
; ;

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US-10-237-866-18
; Sequence 18, Application US/10237866
; Publication No. US20030036171A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
;
; CURRENT APPLICATION DATA: US/10/237,866
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 249 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-866-18
Query Match 61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAELVPGTSTVKISKASGYTFTNTWLGWVKQRPGLHLEWIGDIYPGGGYTNV 62
DB 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMWVVKQRPGLHLEWIGRIYPGDGTKY 63
QY 63 NEKFKGKATVADTSRTAYQVRSITSDSAVYFCARSAS-----WYFDVWGARTTV 115
DB 64 NGKFKGKATLTADRSSSTAYMQLSSLTSGSAVYFCAKENRRFDERGYAMDYWGQGTTV 123
QY 116 TVSSAKTTPKLG-----DIETQSPKEMSTSGVDRVNVYKASONGVNTNVAWFOQKPG 169
DB 124 TVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 183
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DB 184 QSPKLLIYWASTRTGVPDRFTGSGSGTDTFTLTISNVQSEDSADYFCQYSSYPWTFGGG 243

US-10-237-871-18
; Sequence 18, Application US/10237871
; Publication No. US20030036172A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
;
; CURRENT APPLICATION DATA: US/10/237,871
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 249 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-871-18
Query Match 61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAELVPGTSTVKISKASGYTFTNTWLGWVKQRPGLHLEWIGDIYPGGGYTNV 62
DB 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMWVVKQRPGLHLEWIGRIYPGDGTKY 63
QY 63 NEKFKGKATVADTSRTAYQVRSITSDSAVYFCARSAS-----WYFDVWGARTTV 115
DB 64 NGKFKGKATLTADRSSSTAYMQLSSLTSGSAVYFCAKENRRFDERGYAMDYWGQGTTV 123
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QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVVYKASQNVGTNVAMFOOKPG 169  
Db 124 TVSSGGGGGGGGGGGSGNIQLTQSPNSMSTSVGDRVSIITCKASQDVTSAWYQOKPG 183  
QY 170 QSPKVLIIYASVRYSGVPRFTGSGGTDTLTISNVQSEDLAEYFCQQYHYPLTFGGG 229  
Db 184 QSPKLLIYWASTRHTGVPDRFTGSGGTDTLTISNVQSEDSADYFCQQYSSYPWTFGGG 243  
QY 230 TKLEIK 235  
Db 244 TKLEIK 249

## RESULT 8

US-10-237-624-18  
; Sequence 18, Application US/10237624  
; Publication No. US20030082747A1  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; Fournier, Alain  
; Guitton, Jean-Dominique  
; Jung, Gerard  
; Yeh, Patrice  
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
; CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
FILING DATE: 10-Sep-2002  
APPLICATION NUMBER: US/10/237,624  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-JAN-1997  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-JAN-1992  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-237-624-18

Query Match 61.8%; Score 862.5; DB 4; Length 249;  
Best Local Similarity 69.5%; Pred. No. 1.2e-57;  
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;  
QY 3 QVQLQQSGAELVRPQTSVKISKASGYFTFTNWLGNVKQRPCHGLEWIGDIYPGGYTNY 62

Db 4 QVQLQQSGELVYKPGASVKISKASGYAFSRSMNWKORPGQGLEWIGRIYPCDGDTKY 63  
QY 63 NEKFKGKATVTDTSRTAYVQVRSITSDSAVYFCARSAS-----WYFDVWGARTTV 115  
Db 64 NKGFKGKATLTADRSSSTAYMQLSSITSVGSAAVYFCAKENRFDERGIYAMDYWGQGTTV 123  
QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVVYKASQNVGTNVAMFOOKPG 169  
Db 124 TVSSGGGGGGGGGGGSGNIQLTQSPNSMSTSVGDRVSIITCKASQDVTSAWYQOKPG 183  
QY 170 QSPKVLIIYASVRYSGVPRFTGSGGTDTLTISNVQSEDLAEYFCQQYHYPLTFGGG 229  
Db 184 QSPKLLIYWASTRHTGVPDRFTGSGGTDTLTISNVQSEDSADYFCQQYSSYPWTFGGG 243  
QY 230 TKLEIK 235  
Db 244 TKLEIK 249

## RESULT 9

US-10-702-536-18  
; Sequence 18, Application US/10702536  
; Publication No. US20040086976A1  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; Fournier, Alain  
; Guitton, Jean-Dominique  
; Jung, Gerard  
; Yeh, Patrice  
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
; CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.1 (PatentIn)  
CURRENT APPLICATION DATA:  
FILING DATE: 07-Nov-2003  
APPLICATION NUMBER: US/10/702,536  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/797,689  
FILING DATE: 31-JAN-1997  
APPLICATION NUMBER: US 08/256,927  
FILING DATE: 28-JUL-1994  
APPLICATION NUMBER: FR 92/01064  
FILING DATE: 31-JAN-1992  
APPLICATION NUMBER: PCT/FR93/00085  
FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-702-536-18

```
Query Match          61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVPPTSVKISKASGYTFTNYWLVKQRPQGHLEWIGDIYPGGYTNY 62
Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKQRPQGLWIGRIYPGDGTKY 63

QY 63 NEKFKGKATVADTSRTAYVQVRSITSDSAVYFCARGAS-----WVFDVWGARTTV 115
Db 64 NGKFKGKATLTADRSSTAYMQLSLTSVGSAYVFCAKENRDERGYAMDYWGQTTV 123

QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGTNVAWFOOKPG 169
Db 124 TVSSGGGGGGGGGGGSGGSGNIQLTQSPNSMSTSVGDRVSIITCKASQDVTSTVAWYQOKPG 183

QY 170 QSPKVLISASYRYSGVDPDRFTGSGSGTDTLTISNVQSEDLAIEYFCQYHTYPLTFGGG 229
Db 184 QSPKLLIYWASTRHTGTGVPDRFTGSGSGTDTLTISNVQSEDSADYFCQYSSYPWTFGGG 243

QY 230 TKLEIK 235
Db 244 TKLEIK 249
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RESULT 10

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US-10-702-636-18
; Sequence 18, Application US/10702636
; Publication No. US20040086977A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
```

```
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10702,636
FILING DATE: 06-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
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; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-702-636-18
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Query Match          61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVPPTSVKISKASGYTFTNYWLVKQRPQGHLEWIGDIYPGGYTNY 62
Db 4 QVQLQSGPELVKPGASVKISKASGYAFSRSMNWKQRPQGLWIGRIYPGDGTKY 63

QY 63 NEKFKGKATVADTSRTAYVQVRSITSDSAVYFCARGAS-----WVFDVWGARTTV 115
Db 64 NGKFKGKATLTADRSSTAYMQLSLTSVGSAYVFCAKENRDERGYAMDYWGQTTV 123

QY 116 TVSSAKTTPKLG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGTNVAWFOOKPG 169
Db 124 TVSSGGGGGGGGGGGSGGSGNIQLTQSPNSMSTSVGDRVSIITCKASQDVTSTVAWYQOKPG 183

QY 170 QSPKVLISASYRYSGVDPDRFTGSGSGTDTLTISNVQSEDLAIEYFCQYHTYPLTFGGG 229
Db 184 QSPKLLIYWASTRHTGTGVPDRFTGSGSGTDTLTISNVQSEDSADYFCQYSSYPWTFGGG 243

QY 230 TKLEIK 235
Db 244 TKLEIK 249
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RESULT 11

```
US-11-146-077-18
; Sequence 18, Application US/11146077
; Publication No. US20050239167A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Guitton, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/146,077
; FILING DATE: 07-JUN-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
```

FILING DATE: 28-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith Ph.D., Julie K.  
REGISTRATION NUMBER: P-38,619  
REFERENCE/DOCKET NUMBER: ST92006-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3839  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-11-146-077-18

Query Match 61.8%; Score 862.5; DB 6; Length 249;  
Best Local Similarity 69.5%; Pred. No. 1.2e-57;  
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;  
QY 3 QVQLQSGAGLVRPGTSVKISKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTN 62  
Db 4 QVQLQSGAGLVRPGTSVKISKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTN 63  
QY 63 NEKFKGKATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYFDVWGARTTV 115  
Db 64 NGPKGKATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCARSAS-----WYFDVWGARTTV 123  
QY 116 TVSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNTYKASQNVGTNVAWFQKPG 169  
Db 124 TVSSGGGGGGGGGGGSGNSQLTQSPNSMSTSVGDRVNTYKASQNVGTNVAWFQKPG 183  
QY 170 QSPKVLISYASRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQYHTYPLTFGGG 229  
Db 184 QSPKLLIYMASTRHTGVPDRFTGSGGTDFTLTISNVQSEDLAEYFCQYHTYPLTFGGG 243  
QY 230 TKLEIK 235  
Db 244 TKLEIK 249

RESULT 12  
US-10-378-832A-2  
Sequence 2, Application US/10378832A  
Publication No. US2004000533A1  
GENERAL INFORMATION:  
APPLICANT: Her Majesty the Queen in right of Canada, as represented by the Minister  
of National Defence  
APPLICANT: Negata, Leslie P  
APPLICANT: Fulton, R. Elaine  
APPLICANT: Hu, Weigang  
APPLICANT: Alvi, Azhar Z  
TITLE OF INVENTION: No. US2004000533A1el Fusion Protein of Human IgG1 Heavy Chain Co  
FILE REFERENCE: NEL-0013  
CURRENT APPLICATION NUMBER: US/10/378,832A  
CURRENT FILING DATE: 2003-03-05  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 2  
LENGTH: 622  
TYPE: PRT  
ORGANISM: mouse hybridoma cells and human lymphocytes  
US-10-378-832A-2  
Query Match 61.8%; Score 862.5; DB 4; Length 622;  
Best Local Similarity 68.7%; Pred. No. 3.1e-57;  
Matches 171; Conservative 24; Mismatches 43; Indels 11; Gaps 3;  
QY 1 MAQVQLQSGAGLVRPGTSVKISKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTN 60  
Db 60 MAQVQLQSGAGLVRPGTSVKISKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTN 119

Query Match 61.4%; Score 856.5; DB 5; Length 255;  
Best Local Similarity 65.2%; Pred. No. 3.4e-57;  
Matches 172; Conservative 27; Mismatches 52; Indels 13; Gaps 5;  
QY 3 QVQLQSGAGLVRPGTSVKISKASGYTFNTYWLGVKQRPCHGLEWIGDIYPGGGYTN 62  
Db 1 EVKLIVSGGDLVKPGGSLKPFSCAASGPPFNRYAMSWYRQTPKGLWVAFI-SSDGIAYY 59  
QY 63 NEKFKGKATVTADTSSRTAYVQVRSLSLTSSEDSAVYFCAR---SASWYFDVWGARTTVTSS 119  
Db 60 ADSVKGRTTISRDNRNAILYQMSLSRSEDAMTYCARVYYSYDYWGQGTTLTVSS 119  
QY 120 AKTTPKLGDIETQSPKFMSTSVGDRVNTYKASQNVGTNVAWFQKPGSPKLIYSA 179  
Db 120 GGG---GSDIIMTQSPKFMSTSVGDRVNTYKASQNVGTNVAWFQKPGSPKLIYSA 175  
QY 180 SYRYSGVDPDRFTGSGGTDFTLTISNVQSEDLAEYFCQYHTYPLTFGGGTKLEIKRAD 238  
Db 176 SSRNSGVDPDRITGSGGTDFTLTISNVQSEDLAEYFCQYHTYPLTFGGGTKLEIKRAD 232  
QY 239 AAAAGSEQLISEEDLNHHHHH 262  
Db 233 -AAAGSEQLISEEDLNHHHHH 255

RESULT 14  
US-10-096-246-36  
Sequence 36, Application US/10096246  
Publication No. US2003010060A1  
GENERAL INFORMATION:  
APPLICANT: The Minister of National Defence, Government of Canada





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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:55:47 ; Search time 19.0991 Seconds  
(without alignments)  
180.014 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQVQLQSGAEIVRPGETV.....GSEQKLISEEDLNHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_PUB.pep:\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	805.5	57.7	615	6	US-10-512-184-50
2	800	57.3	290	7	US-11-032-773-957
3	793.5	56.9	543	6	US-10-495-664-3
4	790.5	56.7	319	7	US-11-032-773-955
5	779	55.8	269	6	US-10-839-799-109
6	765.5	54.9	245	7	US-11-054-515-1902
7	763.5	54.7	251	7	US-11-054-515-1921
8	760.5	54.5	592	6	US-10-016-686-4
9	759	54.4	248	7	US-11-054-515-1778
10	757.5	54.3	248	7	US-11-054-515-1008
11	755.5	54.2	243	6	US-10-016-686-1
12	755.5	54.2	247	7	US-11-054-515-3242
13	751.5	53.9	488	6	US-10-016-686-3
14	748	53.6	242	7	US-11-054-515-1915
15	747	53.5	244	7	US-11-054-515-1881
16	745	53.4	248	7	US-11-054-515-1446
17	741.5	53.2	249	7	US-11-054-515-926
18	738	52.9	250	7	US-11-054-515-932
19	737.5	52.9	249	7	US-11-054-515-918
20	736	52.8	248	7	US-11-054-515-1104
21	734	52.6	246	7	US-11-054-515-1920
22	731.5	52.4	241	7	US-11-054-515-1577
23	731.5	52.4	249	7	US-11-054-515-1635
24	728.5	52.2	249	7	US-11-054-515-919
25	728	52.2	248	7	US-11-054-515-1717

26 727.5 52.2 243 7 US-11-054-515-2063 Sequence 2063, Ap  
27 727 52.1 242 7 US-11-054-515-1580 Sequence 1580, Ap  
28 727 52.1 246 7 US-11-054-515-2062 Sequence 2062, Ap  
29 726 52.0 248 7 US-11-054-515-1700 Sequence 1700, Ap  
30 726 52.0 248 7 US-11-054-515-1719 Sequence 1719, Ap  
31 726 52.0 248 7 US-11-054-515-1733 Sequence 1733, Ap  
32 726 52.0 248 7 US-11-054-515-1737 Sequence 1737, Ap  
33 726 52.0 248 7 US-11-054-515-1879 Sequence 1879, Ap  
34 725.5 52.0 241 7 US-11-054-515-1948 Sequence 1948, Ap  
35 725.5 51.9 245 7 US-11-054-515-1900 Sequence 1900, Ap  
36 724.5 51.9 248 6 US-10-512-184-36 Sequence 36, Appl  
37 724 51.9 248 7 US-11-054-515-1771 Sequence 1771, Ap  
38 721.5 51.7 241 6 US-10-902-546-6 Sequence 6, Appl  
39 721.5 51.7 245 7 US-11-054-515-1972 Sequence 1972, Ap  
40 718 51.5 248 6 US-10-512-184-48 Sequence 48, Appl  
41 715.5 51.3 247 7 US-11-054-515-969 Sequence 969, Appl  
42 714.5 51.2 257 7 US-11-056-825-10 Sequence 10, Appl  
43 712 51.0 626 6 US-10-512-184-49 Sequence 49, Appl  
44 711.5 51.0 241 6 US-10-902-546-5 Sequence 5, Appl  
45 711.5 51.0 243 7 US-11-054-515-1943 Sequence 1943, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-512-184-50

; Sequence 50, Application US/10512184

; Publication No. US2005024901A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.  
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

; TITLE OF INVENTION: resistance against fungi

; FILE REFERENCE: 3581.01US01

; CURRENT APPLICATION NUMBER: US/10/512,184

; CURRENT FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 50

; LENGTH: 615

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: fusion protein

; OTHER INFORMATION: comprising the leader peptide - chitinase - linker

; OTHER INFORMATION: - scfv S2 - cmc/His6.

; US-10-512-184-50

Query Match 57.7%; Score 805.5; DB 6; Length 615;  
Best Local Similarity 59.6%; Pred. No. 2.1e-48;  
Matches 165; Conservative 35; Mismatches 58; Indels 19; Gaps 6;

Qy 1 MAQVQLQSGAEIVRPGETSVKISCKASGYTFYTNVLGVKVRQPGHLEIGDIYVGGYIT 60  
Db 342 MAQVQLQSGTVLARPAGASVKMSCKASGYTFYTNVHWKVRQPGHLEIGDIYVGGYIT 401

Qy 61 NYNEKPKGKATVADTSSRTAYVQVRSITSDSAVYFCARSASWYF--DVMGARTTVTS 118  
Db 402 SYNQKPKGKAKLTAVTSTSTAYMELSLTSDSAVYCTRT-DWDYAMDYWGQGTSTVTS 460

Qy 119 SAKT-----TPKLGDIELTQSPKFMSTSVGDRVNVITYKASQNVGTNVAWFOOK 167  
Db 461 SGSTSGSGKPGPEGSTGKGPADIVLFQSPVIMASPGKVTMTCSASSV-NIYIYQWK 519

Qy 168 PGQSPKVLIIYSASRYSGVPRFTFGSGSGDTFTLTISNVOSEDLAEPCCQHYVPLTFG 227  
Db 520 SGTSFKRWIYDTSKLAGSGVPVRFSGSGSTFSLTISSEAEADIAITYCQWSSPPLTFG 579

Qy 228 GGTKLEIKRADAAGSEOKLISEEDLNS--HHHHH 262

Db 580 AGTKLEIKRAVDAAA--EQKLISEEDLGALDHHHHH 614

```
RESULT 2
US-11-032-773-957
; Sequence 957, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD SIC5 V5 His protein sequence
US-11-032-773-957

Query Match      57.3%; Score 800; DB 7; Length 290;
Best Local Similarity 58.4%; Pred. No. 2.5e-48;
Matches 170; Conservative 31; Mismatches 60; Indels 30; Gaps 7;

QY      1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGWVKQRPCHGLEWIGDIYPGGGYT 60
D*      1 MAEVQLQSGAEIVKPGASVKISKASGYTFTDHIWVWKQRPQEQGLEWIGFISPGNGDI 60

QY      61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVYFCARSASW-----YFDVWGARTT 116
L6      61 RYNEKFKDQATLTADKSSSTAYMQVLSLTSEDSAVYFCARSFYDDNDYGDYWGQGTTLT 120

QY      117 VSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNVTYKASQNV-----GTNVAMFQK 164
Db      121 VSSS-GAPGGSGGGGGGGSDIVLTQSPALMSASLEERVMTCTASSSVSSSYFHHY 179

QY      165 QQKPGSPKVLISARYSGVDPDRFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPL 224
Db      180 QQKPGSPKLIWYTTNLSAGVPAFPFSGSGSRTDFTLTIDPVEADDAATYCCQNNEDPLTF 239

QY      225 TFGGGTKLEIKRADA-----AAGS-----EQKLISEEDLNS-----HHHHH 262
Db      240 TFGAGTKLEIKRADAAPTVAASFLGKPIPNPLGLDSTNSAVDHHHHH 290

RESULT 3
US-10-495-664-3
; Sequence 3, Application US/10495664
; Publication No. US20050244416A1
; GENERAL INFORMATION:
; APPLICANT: JUNG, GUNDRAM
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE
; FILE REFERENCE: 034258-0801
; CURRENT APPLICATION NUMBER: US/10/495,664
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/EP02/12545
; PRIOR FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: DE 101 56 482.1
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 3.3
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
; OTHER INFORMATION: protein construct
US-10-495-664-3

Query Match      56.9%; Score 793.5; DB 6; Length 543;
Best Local Similarity 59.1%; Pred. No. 1.2e-47;
Matches 162; Conservative 26; Mismatches 55; Indels 31; Gaps 4;

QY      3 QVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGWVKQRPCHGLEWIGDIYPGGGYTNY 62
Db      287 QVKLQSGPELVKPGASVKISKASGYAFSRSMWVWVKQRPQGLEWIGRIYPGDGTNY 346

QY      63 NEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVYFCARS-----ASWYFDVWGARTT 118
Db      347 NGKFKGKATLTADKSSSTAYMQVLSLTSEDSAVYFCARGNTVVVYTDYWGQGTITVS 406

QY      119 SAKTTPKLG-----DIETQSPKFMSTSVGDRVNVTYKASQNV-----GTNVAMFQK 168
Db      407 SGGGGSGGGGGGGSDIETQSPASLAVSLGORATISCRASESDSYGNSFMHWYQK 466

QY      169 QGSPKVLISARYSGVDPDRFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPLTF 228
Db      467 GQPPKLLIYASNLSESGVPAFPFSGSGSRTDFTLTIDPVEADDAATYCCQNNEDPLTF 526

QY      229 GTKLEIKRADAAGSEQKLISEEDLNSHHHHH 262
Db      527 GTKLEIKRAA-----HHHHH 543

RESULT 4
US-11-032-773-955
; Sequence 955, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD SIC5 CD20 His Protein Sequence
US-11-032-773-955

Query Match      56.7%; Score 790.5; DB 7; Length 319;
Best Local Similarity 53.4%; Pred. No. 1.2e-47;
Matches 171; Conservative 31; Mismatches 59; Indels 59; Gaps 7;

QY      1 MAQVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGWVKQRPCHGLEWIGDIYPGGGYT 60
Db      1 MAEVQLQSGAEIVKPGASVKISKASGYTFTDHIWVWKQRPQEQGLEWIGFISPGNGDI 60

QY      61 NYNEKFKGKATVTADTSSRTAYVQVRSLTSEDSAVYFCARSASW-----YFDVWGARTT 116
Db      61 RYNEKFKDQATLTADKSSSTAYMQVLSLTSEDSAVYFCARSFYDDNDYGDYWGQGTTLT 120

QY      117 VSSAKTTPKLG-----DIETQSPKFMSTSVGDRVNVTYKASQNV-----GTNVAMFQK 164
Db      121 VSSS-GAPGGSGGGGGGGSDIVLTQSPALMSASLEERVMTCTASSSVSSSYFHHY 179

QY      165 QQKPGSPKVLISARYSGVDPDRFTGSGSGTDFLTITISNVQSEDLAEYFCQOYHTYPL 224
Db      180 QQKPGSPKLIWYTTNLSAGVPAFPFSGSGSRTDFTLTIDPVEADDAATYCCQNNEDPLTF 239
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QY 225 TFGGKLEIKRADAA-----AAGSEQKL-----ISEEDLN----- 255  
Db 240 TFGAGYKLEIKRADAAFTVSAASFLKISHFLQWESLNFIRAHTPVINIYNCBPANPSEK 299  
QY 256 -----SHHHHHH 262  
Db 300 NSPSTQVCYNSAVDHHHHH 319

RESULT 5  
US-10-839-799-109  
; Sequence 109, Application US/10839799  
; Publication No. US20050249726A1  
; GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshiniko  
; SATO, Koh  
; TSUCHIYA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; MEDULLOBLASTOMA CELLS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/839,799  
; FILING DATE: 06-May-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,265  
; FILING DATE: 09-SEP-1996  
; APPLICATION NUMBER: WO PCT/JP94/01763  
; FILING DATE: 19-OCT-1994  
; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 269 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:  
US-10-839-799-109

Query Match 55.8%; Score 779; DB 6; Length 269;  
Best Local Similarity 61.8%; Pred. No. 6.4e-47;  
Matches 149; Conservative 35; Mismatches 51; Indels 6; Gaps 1;

QY 1 MAQVQLQSGAEELVRPGTSVKISCKASGYTFNTYMWLQVQKRPQGHLEWIGDIYPGGGYT 60  
Db 21 MAQVQLVSGAEVKEKPGSSVKVCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNT 80  
QY 61 NYNEKFKGKATVADTSSRTAYVQVRSITSDSAVYFCARASWYFDVWGARTTTVSSA 120  
Db 81 KYDPKFGQGVITADESTNTAYMELSSLRSEDTAFYFCASAYVYNQDYWGQGTITVTVSSG 140  
QY 121 KITPKLGG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGNTVAVFQKPGQSPKV 174

Db 141 GGGSGGGSGGGGSDIQMTQSPSSLSASVGRDRTITCKASQNVGNTVAVYQKPGKAPK 200  
QY 175 LIYSASYRYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHTYPLTFFGGTKLEI 234  
Db 201 LIYSASYRYSGVPSRPSGSGSGDTFTLTISLQPEDIAITYCQYNSYPRAFQGTKEI 260  
QY 235 K 235  
Db 261 K 261

RESULT 6  
US-11-054-515-1902  
; Sequence 1902, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1902  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1902

Query Match 54.9%; Score 765.5; DB 7; Length 245;  
Best Local Similarity 58.2%; Pred. No. 4.9e-46;  
Matches 142; Conservative 41; Mismatches 50; Indels 11; Gaps 2;

QY 3 QVQLQQSGAEELVRPGTSVKISCKASGYTFNTYMWLQVQKRPQGHLEWIGDIYPGGYNY 62  
Db 1 QMQLVQSGAEVKEKPGASVKVCKASGYTFTSYNHWVRQAPGQGLEWMGLVHPNDGSVNY 60  
QY 63 NEKPKGKATVADTSSRTAYVQVRSITSDSAVYFCARS-----ASWYFDVWGARTTTTV 117  
Db 61 AQKFKGRVTWTRDTSTSTVYMELSLSDDTAVYICARDRSGWPNWYFDLWQGTLLTV 120  
QY 118 SSATKTPKLG-----DIELTQSPKFMSTSVGDRVNVYTKASQNVGNTVAVFQKPGQS 171  
Db 121 SSGGGSGGGSGGGGSDIQMTQSPFSLASIGDRVITCRASEGIYHNLAWYQKPGKA 180  
QY 172 PKVLIYSASYRYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHTYPLTFFGGTK 231  
Db 181 PKLLIYKASSLASGAPSRFSGSGSGDTFTLTISLQPDPAITYCQYSNYPLTFFGGTK 240  
QY 232 LEIK 235  
Db 241 LEIK 244





QY 234 IKR 236  
Db 241 IKR 243

## RESULT 12

US-11-054-515-3242  
; Sequence 3242, Application US/11054515  
; Publication No. US20050255532A1

## ; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 3242

; LENGTH: 247

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-3242

Query Match 54.2%; Score 755.5; DB 7; Length 247;  
Best Local Similarity 58.7%; Pred. No. 2.4e-45;  
Matches 145; Conservative 38; Mismatches 51; Indels 13; Gaps 2;

QY 3 QVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGHWKQRPQGHLEWIGDIYPGGYTNY 62  
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTGLNGYISWVRQAPGGGLEWMAIIPNFGTNY 60

QY 63 NEKFKGKATVTADTSSRTAYQVRSITSDSAVYFCARSA-----WYFDVWGARTTV 115  
Db 61 VQKFGQGVMTTDTSTAYMELRLSRDSTAYVYCARGSSGWYDYIYMDVWGKGTWV 120

QY 116 TVSSAKTTPKLG-----DIETQSPKPMSTSVGDRVNVYKASQNVGTNNVAFQKPG 169  
Db 121 TVSSGGGGGGGGGGGGSDIQMTQSPFSLASIGDRVITCRASEGIYHWLAWYQKPG 180

QY 170 QSPKVLAYSARYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHTYPLTFGGG 229  
Db 181 KAPKLLIYKASSLASGAPRFSGSGGDTFTLTISLQPDDFATYCCQYSNYPLTFGGG 240

QY 230 TKLEIKR 236  
Db 241 TKLEIRR 247

## RESULT 13

US-10-016-686-3

; Sequence 3, Application US/10016686

; Publication No. US2006001422A1

## ; GENERAL INFORMATION:

; APPLICANT: Oxford Biomedica (UK) Limited  
; APPLICANT: Kingsman, Alan  
; APPLICANT: Kingsman, Susan Mary  
; APPLICANT: Bebbington, Christopher Robert  
; APPLICANT: Carroll, Miles William  
; APPLICANT: Ellard, Fiona Margaret  
; APPLICANT: Myers, Kevin Alan  
; TITLE OF INVENTION: Antibodies  
; FILE REFERENCE: 674523-2012  
; CURRENT APPLICATION NUMBER: US/10/016,686  
; CURRENT FILING DATE: 2002-11-02  
; PRIOR APPLICATION NUMBER: PCT/GB00/04317  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 488  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion protein  
US-10-016-686-3

Query Match 53.9%; Score 751.5; DB 6; Length 488;

Best Local Similarity 61.7%; Pred. No. 8.3e-45;

Matches 150; Conservative 28; Mismatches 56; Indels 9; Gaps 2;

QY 2 AQVQLQSGAEIVRPGTSVKISKASGYTFTNYWLGHWKQRPQGHLEWIGDIYPGGYTNY 61  
Db 246 SEVQLQSGPDLVQPGASVKISKASGYFTGYMHVWQSHGKSLIEWIGRINPNNGVTL 305

QY 62 YNEKFKGATVTADTSSRTAYQVRSITSDSAVYFCARS---ASWYFDVWGARTTVTVS 118  
Db 306 YNQKFKDKAILFTVDSSTTAYMELRLTSDSAVYCARSTMITNYMDYWGQVTSVTVS 365

QY 119 S-----AKTTPKLGDELTLQSPKPMSTSVGDRVNVYKASQNVGTNNVAFQKPGQSP 172  
Db 366 SGGGGGGGGTGGGSSIVMTQTPTFLVLSAGDRVTITCKASQSVNDVAVYQKPGQSP 425

QY 173 KVLIIYSARYSGVDPDRFTGSGSGDTFTLTISNVQSEDLAEYFCQYHTYPLTFGGGTKL 232  
Db 426 TLLISVTSRYAGVDPDRFIGSGYGTFTTISTLQAEIDLAVYFCQDYNSPPTFGGGTKL 485

QY 233 EIK 235  
Db 486 EIK 488

## RESULT 14

US-11-054-515-1915

; Sequence 1915, Application US/11054515

; Publication No. US20050255532A1

## ; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; ORGANISM: Homo sapiens
US-11-054-515-1881
Query Match 53.5%; Score 747; DB 7; Length 244;
Best Local Similarity 59.4%; Pred. No. 9e-45;
Matches 145; Conservative 42; Mismatches 47; Indels 10; Gaps 3;
QY 3 QVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWYKQRPQGHLEWIGDIYFGGGYNY 62
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGGTFFSSYAIISWVRQAPGQGLEWMGGIIPFGTANY 60
QY 63 NEKPKGKATVATDTSRTATVQVRSLSDESAVYFCAR-SASWY----FDVWGARTTIVTS 118
Db 61 AQKFGQRTTITADKSTSTAYMELSLRSDDTAVYICARDSGSYYDAFDIWKGTMTVTS 120
QY 119 SAKTTPKLG------DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQSP 172
Db 121 SGGGGGGGGGGGGSDIVMTQSPSTLSASVGRVITCRASQGISWLAWYQOKPGKAP 180
QY 173 KVLIIYSARYISGVPRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYHTYPLTFGGGTXYL 232
Db 181 KLIIYAASSLQSGVPRFSGSGSDTFTLTISLQPEDFATYYCQANSFPLTFGGGTXY 240
QY 233 EIKR 236
Db 241 EIKR 244
Search completed: February 9, 2006, 04:00:31
Job time : 20.0991 secs

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1915
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1915
Query Match 53.6%; Score 748; DB 7; Length 242;
Best Local Similarity 59.9%; Pred. No. 7.6e-45;
Matches 145; Conservative 3; Mismatches 52; Indels 8; Gaps 2;
QY 3 QVQLQSGAELVRPGTSVKISKASGYTFTNYMLGWYKQRPQGHLEWIGDIYFGGGYNY 62
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGGTFFSSYAIISWVRQAPGQGLEWMGGIIPFGTANY 60
QY 63 NEKPKGKATVATDTSRTATVQVRSLSDESAVYFCAR-SASWYF--DVGARTTIVTSSA 120
Db 61 AQKFGQRTTITADKSTSTAYMELSLRSDDTAVYICARGPSYIYMAVWGQGLTIVTSSG 120
QY 121 KTFPKLG------DIELTQSPKFMSTSVGDRVNVYKASQNVGTNVAVFOOKPGQSPKV 174
Db 121 GGGGGGGGGGGGGSDIQTQSPSTLSASVGRVITCRASQGINNYLAWYQOKPGRAPKL 180
QY 175 LIYSASVRYISGVPRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYHTYPLTFGGGTXYL 234
Db 181 LIYAASSLQSGVPRFSGSGSDTFTLTISLQPEDFATYYCQANSFPLTFGGGTXYL 240
QY 235 KR 236
Db 241 KR 242

RESULT 15
US-11-054-515-1881
; Sequence 1881, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1881
; LENGTH: 244
; TYPE: PRT

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:18:06 ; Search time 281.675 Seconds  
(without alignments)  
425.847 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQQSGAELRPGASV.....GSEQLISEDLNHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Geneseq 21:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*
  - 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1470	100.0	273	4 AAB70763	Aab70763 Single ch
2	1231.5	83.8	272	7 ADE22203	Ade22203 Multivale
3	1041.5	70.9	415	2 AAR56484	Aar56484 Scfv PRAS
4	1027.5	69.9	402	2 AAR56485	Aar56485 Scfv PRAS
5	1026.5	69.8	269	2 AAR54756	Aar54756 PRAS111 b
6	1025.5	69.8	269	2 AAR56482	Aar56482 Scfv PRAS
7	1015.5	69.1	256	2 AAR22568	Aar22568 ScfvB18 c
8	1014.5	69.0	256	2 AAR22584	Aar22584 ScfvB18 c
9	1014.5	69.0	256	2 AAR56483	Aar56483 Scfv PRAS
10	1011.5	68.8	435	2 AAR22582	Aar22582 ScfvB18 c
11	1010.5	68.7	428	2 AAR24027	Aar24027 Single ch
12	1010.5	68.7	443	2 AAR24025	Aar24025 Single ch
13	1009.5	68.7	256	2 AAR22587	Aar22587 ScfvB18 c
14	1009.5	68.7	256	2 AAR22585	Aar22585 ScfvB18 c
15	1008.5	68.6	256	2 AAR22586	Aar22586 ScfvB18 c
16	1005.5	68.4	256	2 AAR22583	Aar22583 ScfvB18 c
17	862	58.6	562	6 ABR57059	Abr57059 Plasmid p
18	834.5	56.8	239	8 ADT07625	Adt07625 Polyepiti
19	825	56.1	288	2 AAW58826	Aaw58826 Human CD3
20	824.5	56.1	288	2 AAW82317	Aaw82317 Mouse bis
21	824.5	56.1	288	2 AAW82316	Aaw82316 Mouse OKT
22	821.5	55.9	243	8 ADT07627	Adt07627 Polyepiti
23	807.5	54.9	288	2 AAW82482	Aaw82482 Mouse bis
24	799.5	54.4	539	3 AAY50823	Aay50823 Fv-antibo

25	799.5	54.4	554	3 AAY50822	Aay50822 Fv-antibo
26	786.5	53.5	294	9 ADZ66387	Adz66387 MOP11 ant
27	785.5	53.4	539	9 ADR42630	Adr42630 Mouse ant
28	774	52.7	267	8 ADM32742	Adm32742 Amino aci
29	771.5	52.5	262	4 AAB70762	Aab70762 Single ch
30	759	51.6	240	1 AAB80157	Aap80157 Biosynthe
31	754	51.3	594	9 AER29087	Aeb29087 Immunokin
32	753.5	51.3	264	7 ADE29202	Ade29202 Multivale
33	751	51.1	562	6 ABR57058	Abr57058 Plasmid p
34	739	50.3	574	7 ADE52216	Ades52216 E3Bi prot
35	735	50.0	2606	7 ADE52217	Ades52217 pGLEN-EH3
36	735	50.0	2606	7 ADE52214	Ades52214 pGLEN-EH3
37	730	49.7	288	2 AAW82743	Aaw82743 Fusion pr
38	709	48.2	492	8 ADQ91100	Adq91100 Antibody
39	707	48.1	492	8 ADQ91082	Adq91082 Antibody
40	707	48.1	492	8 ADQ91092	Adq91092 Antibody
41	706	48.0	492	8 ADQ91080	Adq91080 Antibody
42	705	48.0	492	8 ADQ91090	Adq91090 Antibody
43	704	47.9	409	5 ABB07680	Abb07680 MOGxCD3 f
44	704	47.9	409	6 ADA14263	Ada14263 Human MOG
45	704	47.9	492	8 ADQ91106	Adq91106 Antibody

ALIGNMENTS

RESULT 1

AAB70763

ID AAB70763 standard; protein; 273 AA.

AC XX

AA AAB70763;

DT 18-MAY-2001 (first entry)

XX Single chain Fv antibody construct anti-CD30 VL domain protein.

XX Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;  
 KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;  
 KW tumor cell; natural killer cell activation; Hodgkin's disease;  
 KW Reed-Sternberg disease.

XX Synthetic.

XX DE19937264-A1.

XX 15-FEB-2001.

XX 06-AUG-1999; 99DE-01037264.

XX 06-AUG-1999; 99DE-01037264.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;

XX WPI; 2001-184000/19.

XX New Fv-antibody construct, useful for treating Hodgkin and Reed-Sternberg diseases, has binding sites for CD16 receptor and CD30 surface protein.  
 XX Disclosure; Page 11; 18pp; German.  
 XX This invention describes a novel Fv-antibody construct (1) having binding sites for a CD16 receptor and a CD30 surface protein. The invention also describes (1) expression vector encoding (1); (2) transformants containing the vector of (1); (3) preparation of (1) by culturing cells of (2); and (4) kit comprising (1) and/or the vector of (1), and auxiliary reagents such as buffers, solvents, carriers, controls and labels, or their replacements. The products of the invention have cytostatic activity. (1) causes lysis of CD30+, specifically tumor cells. It activates natural killer cells, through the CD16 receptor, and directs them to CD30-expressing cells. (1) are used to treat diseases in which CD30+ cells are implicated, particularly tumors and specifically Hodgkin

CC or Reed-Sternberg diseases. (I) have a stronger lytic action than known  
CC bispecific antibodies, can be produced on a large scale with high purity,  
CC and contain no components that can induce unwanted immune responses  
XX  
SQ Sequence 273 AA;

Query Match 100.0%; Score 1470; DB 4; Length 273;  
Best Local Similarity 100.0%; Pred. No. 4.2e-93;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQVQLQDSGAELARPGASVMSCKASGYTFYTIHWVRQPGHLEWIGYINPSSGYS 60  
DB 1 MAQVQLQDSGAELARPGASVMSCKASGYTFYTIHWVRQPGHLEWIGYINPSSGYS 60  
QY 61 DYNQNFKGKTLTADKSSNTAYMQLNSLTSEDSAVVYCARRADYGNVYTWFAWQGGTT 120  
DB 61 DYNQNFKGKTLTADKSSNTAYMQLNSLTSEDSAVVYCARRADYGNVYTWFAWQGGTT 120  
QY 121 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 180  
DB 121 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 180  
QY 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTDEAIYFCALWYNNHVVFGGTT 240  
DB 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTDEAIYFCALWYNNHVVFGGTT 240  
QY 241 KLTVLGQPKSAAGSQKLISEDLNSHHHHH 273  
DB 241 KLTVLGQPKSAAGSQKLISEDLNSHHHHH 273

RESULT 2  
ADE29203  
ID ADE29203 standard; protein; 272 AA.

XX ADE29203;  
XX 29-JAN-2004 (first entry)  
XX Multivalent multimeric antibody CD19xCD16 related protein 3.  
XX multivalent multimeric antibody; bispecific diabody; BsbD;  
KW human B cell marker; CD19; human Fc gamma receptor III; CD16; cytostatic;  
KW immunosuppressive; B-cell malignancy; non-Hodgkin lymphoma;  
KW B-cell mediated autoimmune disease; B-cell depletion; immune response;  
KW human anti-murine antibody response; CD19 x CD16 BsbD; pSKID19x16; mouse;  
murine.  
XX Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Region 31..35  
FT /label= Complementarity\_determining\_region\_H1  
FT Region 50..66  
FT /label= Complementarity\_determining\_region\_H2  
FT Region 99..113  
FT /label= Complementarity\_determining\_region\_H3  
FT Region 124..133  
FT /label= Synthetic\_linker  
FT Region 158..171  
FT /label= Complementarity\_determining\_region\_L1  
FT Region 187..196  
FT /label= Complementarity\_determining\_region\_L2  
FT Region 226..234  
FT /label= Complementarity\_determining\_region\_L3  
FT Region 255..264  
FT /label= c-myc epitope  
FT Region 267..272  
FT /label= 6xHis\_tag  
XX EP1314741-A1.  
XX 28-MAY-2003.

XX 14-NOV-2001; 2001EP-00127061.  
XX 14-NOV-2001; 2001EP-00127061.  
XX (AFFI-) AFFIMED THERAPEUTICS AG.  
XX Le Gall F, Kipriyanov MS, Moldenhauer G, Little M, Cochlovius B,  
PI Schaefer JH;  
XX WPI; 2003-620028/59.  
DR N-PSDB; ADE29201.  
XX Multivalent multimeric antibody for treating B-cell malignancies such as  
PT non-Hodgkin lymphoma, comprises specificities, and antigen-binding domain  
PT specific to human CD19 and CD16.  
XX  
PS Example 1; SEQ ID NO 3; 38pp; English.  
XX This invention relates to a novel multivalent multimeric antibody (a  
CC bispecific diabody - BsbD) which comprises at least two binding sites  
CC specific for the human B cell marker CD19 and human Fc gamma receptor III  
CC (CD16). The invention may allow the development of compositions with  
CC cytostatic or immunosuppressive activity. The antibody is useful for the  
CC diagnosis and treatment of B-cell malignancies such as non-Hodgkin  
CC lymphoma, B-cell mediated autoimmune diseases or the depletion of B-  
CC cells. The multivalent multimeric antibody avoids the undesired immune  
CC response such as human anti-murine antibody response. The specification  
CC provides a process for stable high yield of recombinant antibodies. The  
CC present sequence is that of a mature mouse derived protein encoded by the  
CC DNA sequence of the CD19 x CD16 BsbD in the expression plasmid pSKID19x16  
CC which was used in the exemplification of the invention.  
XX Sequence 272 AA;  
Query Match 83.8%; Score 1231.5; DB 7; Length 272;  
Best Local Similarity 85.7%; Pred. No. 1e-76;  
Matches 234; Conservative 14; Mismatches 22; Indels 3; Gaps 2;  
QY 3 QVQLQDSGAELARPGASVMSCKASGYTFYTIHWVRQPGHLEWIGYINPSSGYSY 62  
DB 1 QVQLQDSGAELVRPGSSVKISKASGYAFSSYMMWVKRQPGGLEWIGIQIWPGDGDTNY 60  
QY 63 NQNFKGKTLTADKSSNTAYMQLNSLTSEDSAVVYCARR--ADYGNVYTWFAWQGGTT 120  
DB 61 NGKFKGKATLTADSSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYA-MDYWQGGTS 119  
QY 121 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 180  
DB 120 VTVSSAKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSYANWVQKPDH 179  
QY 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTDEAIYFCALWYNNHVVFGGTT 240  
DB 180 LFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTDEAIYFCALWYNNHVVFGGTT 239  
QY 241 KLTVLGQPKSAAGSQKLISEDLNSHHHHH 273  
DB 240 KLTVLGQPKSAAGSQKLISEDLNSHHHHH 272  
RESULT 3  
AAR56484  
ID AAR56484 standard; protein; 415 AA.  
XX AAR56484;  
XX 25-MAR-2003 (revised)  
DT 26-MAR-1995 (first entry)  
XX ScFv pRAS109 and pRAS113.  
XX Amplification; single chain variable region fusion protein; PCR.  
XX

OS Synthetic.  
 XX WO9415644-A1.  
 PN  
 XX  
 XX  
 PD 21-JUL-1994.  
 PF  
 XX 17-JAN-1994; 94WO-GB0000087.  
 XX  
 XX 15-JAN-1993; 93GB-00000686.  
 PR  
 XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 PA  
 XX Epenetos AA, Spooner RA, Deonarain M;  
 XX N-PSDB; AAQ70660.  
 DR WPI; 1994-248907/30.  
 DR N-PSDB; AAQ70660.  
 XX  
 XX New cpds. comprising a targetting portion and a cytotoxic portion - used  
 PT esp. for treating mammals for destroying target cells, partic. tumour  
 PT cells.  
 XX  
 XX Disclosure; Fig 10; 114pp; English.  
 PS  
 XX The sequence is that of the ScFv pRAS109 and pRAS113 between HindIII and  
 CC EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 CC  
 XX Sequence 415 AA;  
 SQ  
 Query Match 70.9%; Score 1041.5; DB 2; Length 415;  
 Best Local Similarity 75.3%; Pred. No. 1.9e-63;  
 Matches 204; Conservative 22; Mismatches 38; Indels 7; Gaps 2;  
 QY 1 MAQVQLQSGAEELARPGASVMSCKASGYTFTTTHHWVRRPGHDLWIGYINPSSGYS 60  
 DB 21 MAQVQLQSGAEELVKPGASVKLSCKASGYTFTSYMEHWVQRPGRGLWIGRIDPSSGGT 80  
 QY 61 DYNQNFKGTTLTADKSNATYMQLSLTSEDSAVYYCARRADYGNVEYTWPAWVGQTT 120  
 DB 81 KYNEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCAR---YDYTGSSYFDYWGQTT 137  
 QY 121 VTSS-----AKTTPKLGSDIQAVVTQESALTTSPGETVTLTCSRNTGTVTTSNYANWVQE 176  
 DB 138 VTSSGGGGGGGGGGGGGSAQVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQE 197  
 QY 177 KPDHLFTGLHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWF 236  
 DB 198 KPDHLFTGLIGTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWF 257  
 QY 237 GGGTKLTVLGQPKSAAGSEQLISEEDLNS 267  
 DB 258 GGGTKLTVLGLEAPAAPADPSKSAQVSA 288  
 RESULT 4  
 AAR56485  
 ID AAR56485 standard; protein; 402 AA.  
 AC  
 AC AAR56485;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 26-MAR-1995 (first entry)  
 DE  
 DE ScFv pRAS110 and pRAS114.  
 XX  
 XX Amplification; single chain variable region fusion protein; PCR.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9415644-A1.  
 PN  
 XX 21-JUL-1994.

PF 17-JAN-1994; 94WO-GB0000087.  
 XX  
 XX 15-JAN-1993; 93GB-00000686.  
 XX  
 XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 PA  
 XX Epenetos AA, Spooner RA, Deonarain M;  
 XX N-PSDB; AAQ70661.  
 DR WPI; 1994-248907/30.  
 DR N-PSDB; AAQ70661.  
 XX  
 XX New cpds. comprising a targetting portion and a cytotoxic portion - used  
 PT esp. for treating mammals for destroying target cells, partic. tumour  
 PT cells.  
 XX  
 XX Disclosure; Fig 11; 114pp; English.  
 PS  
 XX The sequence is that of the ScFv pRAS110 and pRAS114 between HindIII and  
 CC EcoRI site obtd. by PCR. See also AAR56482-4. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 CC  
 XX Sequence 402 AA;  
 SQ  
 Query Match 69.9%; Score 1027.5; DB 2; Length 402;  
 Best Local Similarity 77.7%; Pred. No. 1.7e-62;  
 Matches 202; Conservative 17; Mismatches 34; Indels 7; Gaps 2;  
 QY 1 MAQVQLQSGAEELARPGASVMSCKASGYTFTTTHHWVRRPGHDLWIGYINPSSGYS 60  
 DB 21 MAQVQLQSGAEELVKPGASVKLSCKASGYTFTSYMEHWVQRPGRGLWIGRIDPSSGGT 80  
 QY 61 DYNQNFKGTTLTADKSNATYMQLSLTSEDSAVYYCARRADYGNVEYTWPAWVGQTT 120  
 DB 81 KYNEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCAR---YDYTGSSYFDYWGQTT 137  
 QY 121 VTSS-----AKTTPKLGSDIQAVVTQESALTTSPGETVTLTCSRNTGTVTTSNYANWVQE 176  
 DB 138 VTSSGGGGGGGGGGGGGSAQVVTQESALTTSPGETVTLTCSRSTGPTVTSIYANWVQE 197  
 QY 177 KPDHLFTGLHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWF 236  
 DB 198 KPDHLFTGLIGTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWF 257  
 QY 237 GGGTKLTVLGQPKSAAGSE 256  
 DB 258 GGGTKLTVLGLEAPAAPAE 277  
 RESULT 5  
 AAR54756  
 ID AAR54756 standard; protein; 269 AA.  
 XX  
 XX AAR54756;  
 AC  
 AC AAR54756;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 06-DEC-1994 (first entry)  
 DE  
 DE pRAS111 between HindIII and EcoRI sites.  
 XX  
 XX Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus; Penton fibre;  
 KW Ad5; Fusion sites; PCR; polymerase chain reaction.  
 XX  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH 1. .269  
 FT Protein /label= Single chain Fv fragment 236  
 FT Peptide 1. .22  
 FT Peptide /label= pelB leader peptide  
 FT Protein 23. .142  
 FT Protein /label= heavy chain variable region  
 FT Region 23. .51  
 FT /label= VH FR1



QY 177 KPDLFTGLTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWF 236  
 Db 198 KPDLFTGLTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWF 257  
 QY 237 GGCTKLTVLG 246  
 Db 258 GGGTKLTVLG 267

## RESULT 7

AAR22568

ID AAR22568 standard; protein; 256 AA.

XX AC AAR22568;

XX DT 21-MAY-1992 (first entry)

XX DE ScFvB18 construct.

XX KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;  
 KW specific binding pairs; replicable genetic display package.

XX OS Synthetic.

XX Key Location/Qualifiers

XX FH Misc-difference 103

XX FT /label= mutation

XX FT /note= "Ala -&gt; Val (VL FR3) x 3 "

XX FT Misc-difference 235

XX FT /label= mutation

XX FT /note= "Tyr -&gt; Asp (VL CDR3) x 1 "

XX FT Misc-difference 236

XX FT /label= mutation

XX FT /note= "Ser -&gt; Gly (VL CDR3) x 1 "

XX FT Misc-difference 242

XX FT /label= mutation

XX FT /note= "Gly -&gt; Ser (VL FR4) x 21; or Gly -&gt; Asp (VL FR4) x 3 "

XX FT Misc-difference 245

XX FT /label= mutation

XX FT /note= "Thr -&gt; Ile (VL FR4) x 1 "

XX XX WO9201047-A.

XX XX 23-JAN-1992.

XX XX 10-JUL-1990; 90GB-00015198.

XX XX 10-OCT-1990; 90GB-00015198.

XX XX 19-OCT-1990; 90GB-00022845.

XX XX 12-NOV-1990; 90GB-00024503.

XX XX 06-MAR-1991; 91GB-00004744.

XX XX 15-MAY-1991; 91GB-00010549.

XX XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX XX (MEDI-) MED RES COUNCIL.

XX XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;

XX XX Jackson RH, Holliger KP, Marks JD;

XX XX WPI; 1992-056862/07.

XX XX N-PSDB; AAQ21100.

XX XX Producing members of specific binding pairs - by expression in  
 XX XX recombinant host cells with a secreting replicable genetic display  
 XX XX package.

XX XX Example 38; Fig 44; 209pp; English.

XX XX The sequence is encoded by an antibody scFv fragment directed against 4-  
 CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb against

CC NP were separately amplified and reassembled to form the construct, which  
 CC was then ligated into the fd gene III contg. vector, fdcAT2, derived from  
 CC fdRps/Xh. (See AAQ21095). The clone having the scFvB18 sequence fused in  
 CC frame to gene III was designated fdcAT2scFvB18. Alternatively the  
 CC fragment was cloned into fdOGkan (fdCAT2 with the tet gene replaced by a  
 CC kanamycin resistance gene) to give fdOGkanscFvB18, or into the phagemid  
 CC PHEN1 to create PHEN1- scFvB18. The constructs were used to test the  
 CC effect of using muta- tor strains to increase the diversity of the cloned  
 CC genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1:  
 CC NR9046 mutT1::Tn10 were constructed by pl transduction. After 4 rounds of  
 CC mutation and screening, 40 phage inserts were sequenced. They each  
 CC displayed single mutations in 6 different positions, five being in the  
 CC light chain region. More than 70% of the mutations occurred at positions  
 CC 724 and 725 (of the nucleotide sequence) changing the first Gly in the J  
 CC segment (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The  
 CC mutant fragments had affinities for NP which were comparable to the wild-  
 CC type scFv fragment (20nM). N.B. fdcAT2 is also referred to as fd-tet-DOG1  
 CC and fdOG1. See also AAR21260-307, 309-311; AAR22450, 565-581  
 XX  
 XX SQ Sequence 256 AA;

Query Match 69.1%; Score 1015.5; DB 2; Length 256;

Best Local Similarity 78.7%; Pred. No. 6.7e-62;

Matches 200; Conservative 17; Mismatches 30; Indels 7; Gaps 3;

QY 2 AQVLOQSGAELARPGASVKMSCKASGYTFYTHHVRQRPGRGLEWIGYINPSSGYSD 61

Db 6 AQVLOQSGAELVKPGASVKLSCKASGYTFYSYMHVWVKQRPGRGLEWIGRIDPNSGDK 65

QY 62 YNQNFKKTTLTADKSNNTAYMQLNSLTSDSAVYICARRADYGNVYTFYFAYGQGTTV 121

Db 66 YNEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYICA-RYDYWGQGTTV 122

QY 122 TVSS-----AKTTPKLGDIQAVVTOBSALTSPGETVTLTCRSNTGVTTSNYANWVQEK 177

Db 123 TVSSGGGGGGGGGGGGGQAVGTQESALTSPGETVTLTCRSNTGVTTSNYANWVQEK 182

QY 178 PDHLFTGLTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWF 237

Db 183 PDHLFTGLTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWF 242

QY 238 GGTGKLTVLGQPKSA 251

Db 243 GGTGKLTVLEIKRAA 256

## RESULT 8

AAR22584

ID AAR22584 standard; protein; 256 AA.

XX AC AAR22584;

XX DT 21-MAY-1992 (first entry)

XX XX ScFvB18 construct #3.

XX KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;  
 KW specific binding pairs; replicable genetic display package.

XX OS Synthetic.

XX XX Key Location/Qualifiers

XX FH Misc-difference 236

XX FT /label= mutation

XX FT /note= "Ser -&gt; Gly (VL CDR3) "

XX XX WO9201047-A.

XX XX 23-JAN-1992.

XX XX 10-JUL-1990; 90GB-00015198.

PR 10-JUL-1990; 90GB-00015198.  
 PR 19-OCT-1990; 90GB-00022845.  
 PR 12-NOV-1990; 90GB-00024503.  
 PR 06-MAR-1991; 91GB-00004744.  
 PR 15-MAY-1991; 91GB-00010549.  
 XX  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PA (MEDI-) MED RES COUNCIL.  
 XX  
 PA McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 PI Jackson RH, Holliger KP, Marks JD;  
 XX  
 DR WPI; 1992-056862/07.  
 DR N-PSDB; AAQ23860.  
 XX  
 PT Producing members of specific binding pairs - by expression in  
 PT recombinant host cells with a secreting replicable genetic display  
 PT package.  
 XX  
 XX Example 38; Fig 44; 209pp; English.  
 PS  
 CC The sequence is encoded by an antibody scFv fragment directed against 4-  
 CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb against  
 CC NP were separately amplified and reassembled to form the construct, which  
 CC was then ligated into the fd gene III contg. vector. fdCAT2, derived from  
 CC fdTP8/Xh. (See AAQ21095). The clone having the scFvB18 sequence fused in  
 CC frame to gene III was designated fdCAT2scFvB18. Alternatively the  
 CC fragment was cloned into fdOGkan (fdCAT2 with the tet gene replaced by a  
 CC kanamycin resistance gene) to give fdOGKanscFvB18, or into the phagemid  
 CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test the  
 CC effect of using muta- tor strains to increase the diversity of the cloned  
 CC genes. The strains NR904mutD5: NR9046 mutD5::Tn10 and NR9046mutL:  
 CC NR9046 mutL::Tn10 were constructed by P1 transduction. After 4 rounds of  
 CC mutation and screening, 40 phage inserts were sequenced. They each  
 CC displayed single mutations in 6 different positions, five being in the  
 CC light chain region. More than 70% of the mutations occurred at positions  
 CC 724 and 725 (of the nucleotide sequence) changing the first Gly in the J  
 CC segment (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The  
 CC mutant shown here occurred once. The mutant fragments had affinities for  
 CC NP which were comparable to the wild- type scFv fragment (20nM). N.B.  
 CC fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1. See also AAR21260-  
 CC 307, 309-311; AAR22450, 565-581  
 XX  
 SQ Sequence 256 AA;  
 Query Match 69.0%; Score 1014.5; DB 2; Length 256;  
 Best Local Similarity 78.7%; Pred. No. 7.9e-62;  
 Matches 200; Conservative 16; Mismatches 31; Indels 7; Gaps 3;  
 QY 2 AQVLOQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGYSD 61  
 DB 6 AQVLOQSGAELVKGASVKLSCKASGYTFYSYMHVWVKQRPGRGLEWIGRIDPNSSGGT 65  
 QY 62 YNQNFPGKTTLTADKSNNTAYMQLNSLTSEDSAVVYCARRADYGNYEYTWFAYWGGTTV 121  
 DB 66 YNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCA-RYDYGSSYY--FDYWGOGTTV 122  
 QY 122 TVSS-----AKTTPKLGDIQAVVTQESALTTSPGETVTLTCSRNTGTVTTSYANVQEK 177  
 DB 123 TVSSGGGGGGGGGGGGGQAVVTQESALTTSPGETVTLTCSRSTGAVTTSYANVQEK 182  
 QY 178 PDHLFTGLIGHTNNRPAVGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVF 237  
 DB 183 PDHLFTGLIGHTNNRPAVGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVF 242  
 QY 238 GGTKLTVLGQPKSA 251  
 DB 243 GGKLTIVLEIKRAA 256  
 RESULT 9  
 AAR56483  
 ID AAR56483 standard; protein; 435 AA.

XX AAR56483;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 26-MAR-1995 (first entry)  
 XX  
 DE ScFv pRAS108 and pRAS112.  
 XX  
 KW Amplification; single chain variable region fusion protein; PCR.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9415644-A1.  
 XX  
 PD 21-JUL-1994.  
 XX  
 PF 17-JAN-1994; 94WO-GB0000087.  
 XX  
 PR 15-JAN-1993; 93GB-00000686.  
 XX  
 PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 XX  
 PI Epenetos AA, Spooner RA, Deonarain M;  
 XX  
 DR WPI; 1994-248907/30.  
 DR N-PSDB; AAQ70659.  
 XX  
 PT New cpds. comprising a targetting portion and a cytotoxic portion - used  
 PT esp. for treating mammals for destroying target cells, partic. tumour  
 PT cells.  
 XX  
 PS Disclosure; Fig 9; 114pp; English.  
 XX  
 CC The sequence is that of the ScFv pRAS108 and pRAS112 between HindIII and  
 CC EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 435 AA;  
 Query Match 69.0%; Score 1014.5; DB 2; Length 435;  
 Best Local Similarity 74.2%; Pred. No. 1.4e-61;  
 Matches 201; Conservative 22; Mismatches 41; Indels 7; Gaps 2;  
 QY 1 MAQVLOQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGYVS 60  
 DB 21 MAQVLOQSGAELVKGASVKLSCKASGYTFYSYMHVWVKQRPGRGLEWIGRIDPNSSGGT 80  
 QY 61 DYNQNPFGKTTLTADKSNNTAYMQLNSLTSEDSAVVYCARRADYGNYEYTWFAYWGGTT 120  
 DB 81 KYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCAR---YDYGSSYFDYWGOGTT 137  
 QY 121 TVSS-----AKTTPKLGDIQAVVTQESALTTSPGETVTLTCSRNTGTVTTSYANVQEK 176  
 DB 138 TVSSGGGGGGGGGGGGGQAVVTQESALTTSPGETVTLTCSRSTGAVTTSYANVQEK 197  
 QY 177 KPDHLFTGLIGHTNNRPAVGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVF 236  
 DB 198 KPDHLFTGLIGHTNNRPAVGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVF 257  
 QY 237 GGKTKLTVLGQPKSAAGSEKQLISEDLNS 267  
 DB 258 GGKTKLTVLGLEAPAPAPADPSKDSKAQVSA 288  
 RESULT 10  
 AAR22582  
 ID AAR22582 standard; protein; 256 AA.  
 XX  
 AC AAR22582;  
 XX  
 DT 21-MAY-1992 (first entry)  
 XX  
 DE ScFvB18 construct mutant #1.











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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:28:13 ; Search time 26.5346 Seconds  
(without alignments)  
989.922 Million cell updates/sec

Title: US-10-049-404-3  
Perfect score: 1470  
Sequence: 1 MAQVQLQQSGAELARGASV.....GSEQKLISEEDLNHHHHH 273

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80: \*  
1: Pir1: \*  
2: Pir2: \*  
3: Pir3: \*  
4: Pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.5	41.0	268	A56446	Ig heavy chain V r
2	578	39.3	287	PC4402	pelB leader/Ig hea
3	572	38.9	214	PC4156	Ig lambda chain V
4	562	38.2	113	B54256	Ig lambda-1 chain
5	558	38.0	128	S52450	Ig lambda chain V
6	556	37.8	129	L1MS4E	Ig lambda-1 chain
7	551.5	37.5	112	S06818	Ig lambda chain V
8	536	36.5	113	S06819	Ig lambda chain V
9	531.5	36.2	249	S41374	single chain Fv an
10	528.5	36.0	114	S06822	Ig lambda chain V
11	527.5	35.9	474	G2MS11	Ig gamma-2b chain
12	526	35.8	106	S20554	Ig lambda chain V
13	524.5	35.7	114	S06820	Ig lambda chain V
14	520	35.4	129	L2MS35	Ig lambda-2 chain
15	515	35.0	113	S06821	Ig lambda chain V
16	506.5	34.5	139	P80024	Ig heavy chain pre
17	502	34.1	99	S14592	Ig lambda chain V
18	493.5	33.6	99	PH1089	Ig lambda chain V r
19	493	33.5	140	PH1482	Ig lambda-1 chain
20	492	33.5	116	L1MSV	Ig heavy chain V r
21	492	33.5	119	S20640	Ig lambda chain V
22	491	33.4	97	PH1090	Ig lambda chain V
23	489	33.3	99	S14594	Ig lambda chain V
24	489	33.3	100	PH1088	Ig gamma chain .m
25	482	32.8	246	S38950	Ig gamma-2a chain
26	482	32.8	446	S40295	Ig heavy chain pre
27	481.5	32.8	139	A27609	pl7-6 antibody hea
28	481	32.7	117	JC2269	Ig heavy chain V r
29	480.5	32.7	128	C37267	Ig heavy chain V r

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C;Accession: A56446  
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A;Reference number: A56446; MUID:95229583; PMID:7713873

A;Accession: A56446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <TAN>

A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 41.0%; Score 602.5; DB 2; Length 268;

Best Local Similarity 47.8%; Pred. No. 7.6e-35;

Matches 133; Conservative 45; Mismatches 75; Indels 25; Gaps 7;

QY 1 MAQVQLQQSGAELARGASVYKMSCKASGYFTFTYTHWQRPGHDLWIGYINPSSGYS 60  
DB 1 MAQVQLQESGAELVKGASVKLSCTTSGFNIKDTYHMKVQRPQGLEWIGRIAPANGIT 60  
QY 61 DYNQNFKGKTLTADKSSNTAYMQLNSLTSESAVYVCARRADYGNVEYTWFA-YMGQGT 119  
DB 61 KYDPKFGKATIAADTSSNTAYLQLSLTSEDYAVYCA-----SYLTRYENYWGQGT 114  
QY 120 TVTVSS-----AKTTPKLGDIQAVVTQESA-LTTPSGETVLTCSRNTGTVTTSYANWV 174  
DB 115 TVTVSSGGSGGGSGGGSDIELTQSPAIMSASLGEKVTMSCRASSV---NFIYVY 170  
QY 175 QEKPDHLFTGLIGHTNNRAPGVPARFSGSLIGKAAITITCAQTEDAIIYFCALWYNNHW 234  
DB 171 QOKSDASPKLWVYVTSHLPGVPAFSGSGSGNSYSLTSSMEGEDAATYTCQOFTSPF 230

QY 235 VFGGTHKLTIVLGPKSNA-----AGSEQKLISEEDLN 266

DB 231 TFGSGTKLEI---KRSAAHHHHHGAABQKLISEEDLN 265

RESULT 2

PC4402

pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein

C;Species: synthetic

C;Date: 06-Nov-1998 #sequence\_revision 06-Nov-1998 #text\_change 06-Nov-1998

C;Accession: PC4402

R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-329, 1997

A;Title: Construction, bacterial expression, and characterization of haptten-specific si

A;Reference number: PC4402



A:Molecule type: protein  
A:Residues: '2', 21-25, 'Q', 27-129 <APP>  
A:Cross-references: UNIPARC:UPI0000173722  
A:Accession: C93775  
A:Molecule type: protein  
A:Residues: 20-129 <AP2>  
A:Cross-references: UNIPARC:UPI0000173722  
A:Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E  
R;Casari, I.M.; Weigert, M.  
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973  
A:Title: Mouse lambda-chain sequences.  
A:Reference number: A93784; MUID:73229669; PMID:4516208  
A:Contents: J558; S104; S178  
A:Accession: A93784  
A:Molecule type: protein  
A:Residues: 20-129 <CE3>  
A:Cross-references: UNIPARC:UPI0000173723  
A:Accession: B93784  
A:Molecule type: protein  
A:Residues: 20-129 <CE2>  
A:Cross-references: UNIPARC:UPI0000173723  
A:Accession: C93784  
A:Molecule type: protein  
A:Residues: 20-43, 'N', 45-70, 'N', 72-115, 'R', 117-129 <CE3>  
A:Cross-references: UNIPARC:UPI0000173723  
A:Note: these proteins were isolated from serum or urine of tumor-bearing mice  
R;Bernard, O.; Hozumi, N.; Tonegawa, S.  
Cell 15, 1133-1144, 1978  
A:Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch  
A:Reference number: A90780; MUID:79084170; PMID:103630  
A:Contents: H2020  
A:Accession: A90780  
A:Molecule type: DNA  
A:Residues: 1-43, 'T', 45-50, 'G', 52-58, 'E', 60-89, 'D', 91-129 <BER>  
A:Cross-references: UNIPARC:UPI0000270B5  
A:Note: the sequence was determined from the differentiated gene  
R;Bothwell, A.L.M.; Paikind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.  
Nature 298, 380-382, 1982  
A:Title: Somatic variants of murine immunoglobulin lambda light chains.  
A:Reference number: A93282; MUID:82220143; PMID:6283385  
A:Contents: S43  
A:Accession: C93282  
A:Molecule type: DNA  
A:Residues: 1-58, 'E', 60-89, 'D', 91-98, 'T', 100-105, 'W', 107-129 <BOT>  
A:Cross-references: UNIPARC:UPI00000270B7  
A:Note: the sequence was determined from the differentiated gene  
C;Comment: The MOPC 104E sequence is shown.  
C;Genetics:  
A;Introns: 16/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; pyroglutamic acid  
F;1-19/Domain: signal sequence #status experimental <SIG>  
F;1-19/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>  
F;34-111/Domain: immunoglobulin homology <IMM>  
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;41-109/Disulfide bonds: #status predicted

Query Match 37.8%; Score 556; DB 1; Length 129;  
Best Local Similarity 92.1%; Pred. No. 5.6e-32;  
Matches 105; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 133 GGDQAVVQBSALTTSPGETVTLTCRSNTGVTTSNYANVWQKPDHLFTGLIGHTNNR 192

Db 16 GAISGAVVQBSALTTSPGETVTLTCRSNTGVTTSNYANVWQKPDHLFTGLIGHTNNR 75

Qy 193 APGVPARPFGSLIGDKAALTTGAQTEDEALYFCALWYNNHWVFGGKTLTVLG 246

Db 76 APGVPARPFGSLIGDKAALTTGAQTEDEALYFCALWYNNHWVFGGKTLTVLG 129

RESULT 7

S06818  
Ig lambda chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C;Accession: S06818  
R;Miller III, A.; Glasel, J.A.  
J. Mol. Biol. 209, 763-778, 1989  
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor  
A:Reference number: S06815; MUID:90064531; PMID:2555519  
A:Accession: S06818  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-112 <MIL>  
A:Cross-references: UNIPARC:UPI000017683F  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 37.5%; Score 551.5; DB 2; Length 112;  
Best Local Similarity 93.8%; Pred. No. 9.8e-32;  
Matches 105; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Qy 138 AVVTQESA-LTTSPEGTVTLTCRSNTGVTTSNYANVWQKPDHLFTGLIGHTNNRPGV 196

Db 1 AVVTQESAXLTTSPGETVTLTCRSNTGVTTSNYANVWQKPDHLFTGLIGHTNNRPGV 60

Qy 197 PARFSGSLIGDKAALTTGAQTEDEALYFCALWYNNHWVFGGKTLTVLQGP 248

Db 61 PARFSGSLIGNKALTTGAQTEDEALYFCALWYNNHWVFGGKTLTVLQGP 112

RESULT 8

S06819  
Ig lambda chain V region (clone 10C3) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 11-Nov-1994 #text\_change 21-Jan-2000  
R;Miller III, A.; Glasel, J.A.  
J. Mol. Biol. 209, 763-778, 1989  
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor  
A:Reference number: S06815; MUID:90064531; PMID:2555519  
A:Accession: S06819  
A:Molecule type: mRNA  
A:Residues: 1-113 <MIL>  
A:Cross-references: UNIPARC:UPI0000115E3C; EMBL:X17168; NID:G52251; PIDN:CAA35046.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;14-91/Domain: immunoglobulin homology <IMM>  
F;21-89/Disulfide bonds: #status predicted

Query Match 36.5%; Score 536; DB 2; Length 113;  
Best Local Similarity 94.4%; Pred. No. 1.2e-30;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 138 AVVTQESALTTSPGETVTLTCRSNTGVTTSNYANVWQKPDHLFTGLIGHTNNRPGV 197

Db 1 AVVTQESALTTSPGETVTLTCRSNTGVTTSNYANVWQKPDHLFTGLIGHTNNRPGV 60

Qy 198 ARFSGSLIGDKAALTTGAQTEDEALYFCALWYNNHWVFGGKTLTVL 245

Db 61 ARFSGSLIGDKAALTTGAQTEDEALYFCALWYNNHWVFGGKTLTVL 108

RESULT 9

S41374  
single chain Fv antibody - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: S41374  
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A;Description: Construction and functional characterization of a single chain Fv antib  
A;Reference number: S41374



```
Db 19 SEVLOQSGPELVNPGASVMSCKASGYTFITVMHVVVKQKPGGLEWIGYINPNKDGTK 78
QY 62 YNQNFKGTWLTADKSNNTAYMOLNSLTSDSAVYVCARRADYGNVYTWFAVWGQGTTV 121
Db 79 FNEKPKGKATLTSKSNNTAYMELSSLTSDSAVYICAR-----DYDYDFWFAWGQGTIV 133
QY 122 TVSSAKTTPKLGDDIQAVVTQESALTTSPGETVLTLCRSNTGTVTTS 168
Db 134 TVSAAKTTP-----PSVYPLAPG-----CGDITGSSVTS 162

RESULT 12
S20654
Ig lambda chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S20654
R/Losman, M.; Faay, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A/Reference number: S20639
A/Accession: S20654
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-106 <LOS>
A/Cross-references: UNIPARC:UPI0000116029; EMBL:X65012; NID:G52705; PIDN:CAA46145.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 35.8%; Score 526; DB 2; Length 106;
Best Local Similarity 93.4%; Pred. No. 5.4e-30;
Matches 99; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 137 QAVVTQESALTTSPGETVLTLCRSNTGTVTTSNVANVQEKPDHLFTGLIGHTNNRPGV 196
Db 1 QAVVTQESALTTSPGETVLTLCRSIGAVTTSNAYVQEKPDHLFTGLIGTNNRPGV 60
QY 197 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKL 242
Db 61 PVRFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKL 106

RESULT 13
S06820
Ig lambda chain V region (clone 12D4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C/Accession: S06820
R/Miller III, A.; Glaseel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A/Reference number: S06815; MUID:90064531; PMID:2555519
A/Accession: S06820
A/Molecule type: mRNA
A/Residues: 1-114 <MIL>
A/Cross-references: UNIPARC:UPI0000176812; EMBL:X17169
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>
F:22-90/Disulfide bonds: #status Predicted

Query Match 35.7%; Score 524.5; DB 2; Length 114;
Best Local Similarity 93.6%; Pred. No. 7.4e-30;
Matches 102; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 138 AVVTQES-ALTTSPGETVLTLCRSNTGTVTTSNVANVQEKPDHLFTGLIGHTNNRPGV 196
Db 1 AVVTQESIXLTLSPEGETVLTLCRSIGAVTTSNAYVQEKPDHLFTGLIGTNNRPGV 60
QY 197 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKLTVL 245
Db 61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHVVFGGTKLTVL 109
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## RESULT 14

L2MS35

Ig lambda-2 chain precursor V region (MOPC 315) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1980 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004

C/Accession: A93431; B93282; B91462; A90372; A90410; S09391; A01997

R/Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.

Nucleic Acids Res. 10, 3831-3843, 1982

A/Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene

A/Reference number: A93431; MUID:82274221; PMID:6287422

A/Accession: A93431

A/Molecule type: mRNA

A/Residues: 1-129 <WUG>

A/Cross-references: UNIPROT:P01729; UNIPARC:UPI00000270BD

R/Bothwell, A.L.M.; Paekind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore,

Nature 298, 380-382, 1982

A/Title: Somatic variants of murine immunoglobulin lambda light chains.

A/Reference number: A93282; MUID:82220143; PMID:6283385

A/Accession: B93282

A/Molecule type: DNA

A/Residues: 1-129 <BOT>

A/Cross-references: UNIPARC:UPI00000270BD

A/Note: the sequence was determined from the differentiated gene

R/Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.

Fed. Proc. 38, 1839-1845, 1979

A/Title: Structure and function of immunoglobulin genes and precursors.

A/Reference number: A91462; MUID:79148758; PMID:428562

A/Accession: B91462

A/Molecule type: protein

A/Residues: 1-22 <SCH>

A/Cross-references: UNIPARC:UPI0000173724

R/Dugan, E.S.; Bradehaw, R.A.; Simms, E.S.; Eisen, H.N.

Biochemistry 12, 5400-5416, 1973

A/Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).

A/Reference number: A90372; MUID:74048693; PMID:4760498

A/Accession: A90372

A/Molecule type: protein

A/Residues: 20-24 'E', 26-73 'D', 75-129 <DUG>

A/Cross-references: UNIPARC:UPI0000173725

R/Gavish, M.; Zakut, R.; Wilchek, M.; Glivol, D.

Biochemistry 17, 1345-1351, 1978

A/Title: Preparation of a semisynthetic antibody.

A/Reference number: A90410; MUID:78187254; PMID:418802

A/Accession: A90410

A/Molecule type: protein

A/Residues: 1-129 <GAV>

A/Cross-references: UNIPARC:UPI00000270BD

R/Bogen, B.; Lambris, J.D.

EMBO J. 8, 1947-1952, 1989

A/Title: Minimum length of an idiotypic peptide and a model for its binding to a major

A/Reference number: S09391; MUID:90005397; PMID:2792076

A/Accession: S09391

A/Molecule type: protein

A/Residues: 110-126 <BOG>

A/Cross-references: UNIPARC:UPI0000173726

C/Comment: This chain is from a myeloma protein with anti-DNP activity.

C/Superfamily: immunoglobulin heterotetramer subunit consists of two identical light (k)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; pyroglutamic acid

F:1-19/Domain: signal sequence #status experimental <SIG>

F:20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>

F:34-111/Domain: immunoglobulin homology <IMM>

F:110-126/Region: idio type to histocompatibility complex class II #status experimental

F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim

F:41-109/Disulfide bonds: #status Predicted

Query Match 35.4%; Score 520; DB 1; Length 129;

Best Local Similarity 85.1%; Pred. No. 1.8e-29;

Matches 97; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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QY 133 GGDIAVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWVQEKPDHLFTGLIGHTNNR 192
Db 16 GASSQAVVTQESALTTSPGGTVLTCRSSTGAVTTSNYANWIOEKPDHLFTGLIGTSNR 75
QY 193 APOVPAVRFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246
Db 76 APOVPAVRFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

RESULT 15
S06821
Ig lambda chain V region (clone 11C7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C:Accession: S06821
R:Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morph
A:Reference number: S06815; MUID:90064531; PMID:2555519
A:Accession: S06821
A:Molecule type: mRNA
A:Residues: 1-113 <MIL>
A:Cross-references: UNIPARC:UPI000115E3E; EMBL:X17170; NID:G52253; PIDN:CAA35048.1; PID
A>Note: the authors translated the codon AGT for residue 47 as Gly, GTT for residue 56 a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer, immunoglobulin
F:14-91/Domain: immunoglobulin homology <IMM>
F:21-89/Disulfide bonds: #status predicted

Query Match 35.0%; Score 515; DB 2; Length 113;
Best Local Similarity 86.6%; Pred. No. 3.4e-29;
Matches 97; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 138 AVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWVQEKPDHLFTGLIGHTNNRAPGVP 197
Db 1 AVVTQESILTTSPGETVTLTCRSSTGAVTTSNYANWVQKPDHLFTSLIGGISNRVPGVP 60
QY 198 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLGQPK 249
Db 61 ARFSGSLIGDKVALTITGTQTEDEAIYFCALWYNSNHLVFGGKTLTVLQPE 112
```

Search completed: February 9, 2006, 03:34:19  
Job time : 27.5346 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: February 9, 2006, 03:18:36 ; Search time 167.882 Seconds  
(without alignments)  
1147.288 Million cell updates/sec  
Title: US-10-049-404-3  
Perfect score: 1470  
Sequence: 1 MAQVQLQSGAEALRPGASV.....GSEQKLISEEDLNHHHHH 273

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	597	40.6	243	2	Q7TQM2_MOUSE
2	590	40.1	487	2	Q65ZL2_MOUSE
3	559	38.0	129	1	LVID_MOUSE
4	557	37.9	129	1	LWIE_MOUSE
5	556	37.8	129	1	LWIB_MOUSE
6	555	37.8	110	1	LVIC_MOUSE
7	548.5	37.3	113	2	Q8CGS1_MOUSE
8	545	37.1	129	2	Q8VDE2_MOUSE
9	539	36.7	255	2	Q6KB05_MOUSE
10	538.5	36.6	109	2	Q9ET13_MOUSE
11	533	36.3	244	2	Q65ZC8_HUMAN
12	520	35.4	129	1	LVB2_MOUSE
13	519.5	35.3	473	2	Q9D81A_MOUSE
14	512.5	34.9	617	2	Q4KML5_MOUSE
15	510	34.7	241	2	Q921A6_MOUSE
16	499	33.6	468	2	Q569W9_MOUSE
17	494.5	33.6	117	1	LV1A_MOUSE
18	490	33.3	120	1	HV03_MOUSE
19	487	33.1	240	2	Q65ZC9_HUMAN
20	481	32.7	472	2	Q6PJA7_MOUSE
21	480	32.7	140	1	HV02_MOUSE
22	479.5	32.6	463	2	Q99LC4_MOUSE
23	479	32.6	616	2	Q504M7_MOUSE
24	478.5	32.6	465	2	Q8PJB2_MOUSE
25	476	32.4	470	2	Q7TMK1_MOUSE
26	472	32.1	168	2	Q8VDC9_MOUSE
27	472	32.1	458	2	Q5BJZ2_RAT
28	469.5	31.9	613	2	Q8VCX7_MOUSE
29	468.5	31.9	489	2	Q8VCX4_MOUSE
30	466.5	31.7	139	1	HV07_MOUSE
31	466	31.7	134	2	Q65ZRC_MOUSE

32	465.5	31.7	145	2	Q924Q7_MOUSE	Q924q7 mus musculus
33	463.5	31.5	142	2	Q924Q1_MOUSE	Q924q1 mus musculus
34	463.5	31.5	146	2	Q924Q3_MOUSE	Q924q3 mus musculus
35	463.5	31.5	146	2	Q924R8_MOUSE	Q924r8 mus musculus
36	463	31.5	482	2	Q8K172_MOUSE	Q8k172 mus musculus
37	462	31.4	117	1	LV2A_MOUSE	P01728 mus musculus
38	461	31.4	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculus
39	461	31.4	117	2	Q924R7_MOUSE	Q924r7 mus musculus
40	461	31.4	143	2	Q924R4_MOUSE	Q924r4 mus musculus
41	459.5	31.3	248	2	Q65ZQ7_MOUSE	Q65zq7 mus sp. b3(
42	459.5	31.3	590	2	Q4V9V8_MOUSE	Q4v9v8 mus musculus
43	459	31.2	143	2	Q924Q5_MOUSE	Q924q5 mus musculus
44	457.5	31.1	477	2	Q58E56_MOUSE	Q58e56 mus musculus
45	457	31.1	138	1	HV48_MOUSE	P03980 mus musculus

ALIGNMENTS

RESULT 1  
Q7TQM2\_MOUSE  
ID Q7TQM2\_MOUSE PRELIMINARY; PRT; 243 AA.  
AC Q7TQM2; 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE ScFv 6H8 protein (Fragment).  
GN Name-scFv 6H8;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/C;  
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;  
RA Peter J.C., Eftekhar P., Billiald P., Wallukat G., Hoebeke J.;  
RT "scFv single chain antibody variable fragment as inverse agonist for  
RT the beta-2 adrenergic receptor";  
RL J. Biol. Chem. 278:36740-36747(2003).  
RL EMBL; AJ574851; CAB00495.1; -; Genomic\_DNA.  
DR HSSP; P01751; 1A6W.  
DR SMR; Q7TQM2; 1-236.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGv; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 1  
SQ SEQUENCE 243 AA; 25976 MW; BEFFP64D2DCF4F76 CRC64;  
Query Match 40.6%; Score 597; DB 2; Length 243;  
Best Local Similarity 47.3%; Pred. No. 2.6e-39;  
Matches 131; Conservative 29; Mismatches 77; Indels 40; Gaps 6;  
Qy 3 QVQLQSGAEALRPGASVKMSCKASGYTFYTIHWVRQRPHGLDWIGINPSSGSDY 62  
Db 1 QVQLQSGSELVRFPGASVKLSCKASGYTFYIHWVWVQRHGGQGLEWIGNIPGSGITNY 60  
Qy 63 NQNFPGKTTLTADKSSNTAYMQLNSLTSEDSAVVYCCARRADYGNVYTFWYFWGQGTVT 122  
Db 61 DEKFKNKGLITVDTSSTAYMHLSSLASEDSAVVYCARGG-----RGLDVGAGTTLT 113  
Qy 123 VSSAKTTPKLG-----DIQAVTQSSALTSGETVTLTCRSNTGVITTSNYANWQE 176  
Db 114 VSSGGGGGGGGGGGGSDIQ-MTQSSSSFSVSLGDRVTITCKASEDIY---NRLAWQQ 169  
Qy 177 KPDHLFTGLIGHTNRPAGVPEAFPSGLIGPKAALTITGAQTEDEAIYFCALWYNNHWVF 236  
Db 170 KPGNAPRLISGATSLGTGVPSRFGSGSGKDYILTSITSLQTEDVATYCCQYWSTR-TF 228  
Qy 237 GGGTKLTVLGQPKSAAGSEQKLISEEDLNHHHHH 273  
|||||



CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC HSSP; P01724; 1A6V.  
 CC SNR; P01727; 20-129.  
 CC DR Ensembl; ENSMUSG0000064012; Mus musculus.  
 CC DR InterPro; IPR007110; Ig-like.  
 CC DR InterPro; IPR003596; Ig\_v.  
 CC DR SMART; SM00406; IGV; 1.  
 CC DR PROSITE; PS0835; IG\_LIKE; 1.  
 CC KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
 CC FT CHAIN 1 19  
 CC FT DOMAIN 20 129 Ig lambda-1 chain V region S43.  
 CC FT NON\_TER 129 129 Ig-like.  
 CC SQ SEQUENCE 129 AA; 13529 MW; 84E54ED7DD5791345 CRC64;

Query Match 37.9%; Score 557; DB 1; Length 129;  
 Best Local Similarity 92.1%; Pred. No. 1.8e-36;  
 Matches 105; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 133 GGDIAVVTQESALTTSPGETVTLTCRSNTGCTVTTSNYANWVQEKDPHLFTGLIGHTNNR 192  
 Db 16 GAISQAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKDPHLFTGLIGTNNR 75

QY 193 APGVPAFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246  
 Db 76 APGVPAFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

## RESULT 5

LV1B\_MOUSE STANDARD; PRT; 129 AA.  
 AC P01724;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 precursor.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 CC Muroidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP PROTEIN SEQUENCE OF 1-29 (MOPC 104E), AND SEQUENCE REVISION TO 20 AND 26.  
 RX MEDLINE=77148916; PubMed=403522;  
 RA Burstein Y., Schechter I.;  
 RT "Amino acid sequence of the NH2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda1-type and kappa-type light chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).  
 [2]  
 RP PROTEIN SEQUENCE OF 20-129 (MOPC 104E AND RPC 20).  
 RX MEDLINE=71107854; PubMed=5276767;  
 RA Appella B.;  
 RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).  
 [3]  
 RP PROTEIN SEQUENCE OF 20-129 (J558 AND S104).  
 RX MEDLINE=73229669; PubMed=4516208;  
 RA Cesari I.M., Weigert M.;  
 RT "Mouse lambda-chain sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).  
 CC -1- MISCELLANEOUS: Compositions and partial sequences of RPC 20 show no differences from MOPC 104E. The sequences of J558 and S104 seems identical with that shown.  
 CC -1- MISCELLANEOUS: These proteins were isolated from serum or urine of tumor-bearing mice.  
 CC -1- MISCELLANEOUS: The MOPC 104E precursor was synthesized in a cell-free system directed by mRNA isolated from MOPC 104E myeloma polyclones. Met-1 was lacking in 90% of the chains. It is probably rapidly cleaved after synthesis.

CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

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CC PIR; B93815; L1MS4E.

DR PDB; 1A6U; X-ray; L=21-128.

DR PDB; 1A6V; X-ray; L/M=N=20-128.

DR PDB; 1A6W; X-ray; L=21-128.

DR Ensembl; ENSMUSG0000064012; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG\_LIKE; 1.

KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;

KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.

FT SIGNAL 1 19

FT CHAIN 20 129 Ig lambda-1 chain V regions MOPC

FT DOMAIN 20 125 Ig-like.

FT MOD\_RES 20 20 Pyroglutamate carboxylic acid.

FT NON\_TER 129 129

FT STRAND 23 25

FT STRAND 28 31

FT TURN 33 34

FT STRAND 36 43

FT TURN 44 45

FT STRAND 46 46

FT HELIX 50 52

FT STRAND 55 60

FT TURN 61 63

FT STRAND 64 70

FT TURN 71 73

FT STRAND 74 75

FT TURN 77 78

FT TURN 81 82

FT STRAND 83 88

FT TURN 89 90

FT STRAND 91 97

FT HELIX 101 103

FT STRAND 105 112

FT STRAND 117 119

FT STRAND 123 127

SQ SEQUENCE 129 AA; 13479 MW; 03629939D5791AC0 CRC64;

Query Match 37.8%; Score 556; DB 1; Length 129;

Best Local Similarity 92.1%; Pred. No. 2.1e-36;

Matches 105; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 133 GGDIAVVTQESALTTSPGETVTLTCRSNTGCTVTTSNYANWVQEKDPHLFTGLIGHTNNR 192

Db 16 GAISQAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKDPHLFTGLIGTNNR 75

QY 193 APGVPAFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 246

Db 76 APGVPAFSGSLIGDKAALITGAQTEDEAIYFCALWYNNHWVFGGKTLTVLG 129

## RESULT 6

LV1C\_MOUSE STANDARD; PRT; 110 AA.

ID LV1C\_MOUSE

AC P01725;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig lambda-1 chain V region S178.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

CC Muroidae; Muridae; Murinae; Mus.

```
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=73229669; PubMed=4516208;
RA Cesari I.M., Weigert M.;
RT "Mouse lambda-chain sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
CC -I- MISCELLANEOUS: This protein was isolated from serum or urine of
CC tumor-bearing mice.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01724; 1A6V.
DR SMR; P01725; 1-110.
DR Ensembl; ENSMUSG0000064012; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 106
FT NON_TER 110 110
FT SEQUENCE 110 AA; 11654 MW; 7D06718E1A530206 CRC64;

Query Match 37.8%; Score 555; DB 1; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.1e-36;
Matches 104; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 137 QAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNRPGV 196
DB 1 QAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNRPGV 60

OY 197 PARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 246
DB 61 PARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 110

RESULT 7
Q8CGS1 MOUSE
ID Q8CGS1_MOUSE PRELIMINARY; PRT; 113 AA.
AC Q8CGS1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
DE Anti-deoxynivalenol scFv lambda light chain variable region
DE (Fragment).
GN Names=Igl-V1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY151141; AA075453.1; -; mRNA.
DR HSSP; P01724; 1A6V.
DR SMR; Q8CGS1; 1-113.
DR Ensembl; ENSMUSG0000064012; Mus musculus.
DR MGI; MGI:96530; Igl-V1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 113
FT SEQUENCE 113 AA; 11654 MW; 7D06718E1A530206 CRC64;

Query Match 37.1%; Score 545; DB 2; Length 129;
Best Local Similarity 90.4%; Pred. No. 1.6e-35;
Matches 103; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 133 GGDIOAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNR 192
DB 16 GAISQAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNR 75

OY 193 AFGVPAFPFGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 246
DB 76 AFGVPAFPFGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 129

RESULT 9
Q6KB05 MOUSE
ID Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
FT NON_TER 113
SQ SEQUENCE 113 AA; 12034 MW; 0C4E4C65597E22BE CRC64;

Query Match 37.3%; Score 548.5; DB 2; Length 113;
Best Local Similarity 92.9%; Pred. No. 7.2e-36;
Matches 105; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

OY 137 QAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNRPGV 196
DB 1 QAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNRPGV 60

OY 197 PARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 248
DB 61 PARFSGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 113

RESULT 8
Q8VDE2 MOUSE
ID Q8VDE2_MOUSE PRELIMINARY; PRT; 129 AA.
AC Q8VDE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin lambda chain variable region (Fragment).
GN Name=Igl-V1; Synonyms=4G12-A-H10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Melle G.;
RL Thesis (1995), Department of Ecole Supérieure de Technicien en
RL Biologie Biochimie, Université Catholique de Lyon, Lyon, France.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Blachere T.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ291694; CAC82790.1; -; mRNA.
DR HSSP; P01724; 1A6V.
DR SMR; Q8VDE2; 20-129.
DR MGI; MGI:96530; Igl-V1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 129
FT NON_TER 129 129
FT SEQUENCE 129 AA; 13565 MW; C07F71003803ADBE CRC64;

Query Match 37.1%; Score 545; DB 2; Length 129;
Best Local Similarity 90.4%; Pred. No. 1.6e-35;
Matches 103; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 133 GGDIOAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNR 192
DB 16 GAISQAVVTQESALTSPGETVTLTCRSNTGVTTSNYANWQKPDHFLTGLIGHTNNR 75

OY 193 AFGVPAFPFGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 246
DB 76 AFGVPAFPFGSLIGDKAALITGAQTEDEAIYFCALWYNNH-VVFGGTKLTVLG 129

RESULT 9
Q6KB05 MOUSE
ID Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE SCFV B8E5 protein (Fragment).
GN Name=SCFV B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RT monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
SQ
Query Match 36.7%; Score 539; DB 2; Length 255;
Best Local Similarity 41.3%; Pred. No. 1.1e-34;
Matches 116; Conservative 39; Mismatches 90; Indels 36; Gaps 6;
QY 3 QVQLQSGAEIARPGASVKMSCKASGYTFYTHHWVRQRPGLDLEWIGINPSSGYSY 62
DB 1 QVQLQSGDLVLPFGSLKVKSCRAAGFTFSYSGMSWVRQTPDKRLKLEWVATISGGSYTY 60
QY 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVYCYARRADYGNIEYTW-FAYWQGTTV 121
DB 61 PDSVKGRFTISRDNAKNTLYLQMSLSKASEDTAMYICARHI--NRYDGAFFYWGQGTTL 117
QY 122 TVSSAKTTPKLG-----DIQAVVQESALTTPSPGTVTLTCSRNTGTTT---SNYAN 172
DB 118 TVSSGGGGSGGGSGGGSDI-VNAQSPSSLSVSAAGEKVMKSCSSQSLNSRNQKNYLA 176
QY 173 WVEKPHLFTGLIHTNNRAGVPAPRPSGLIGDKAALTITGAQTEDEALYFCALWYNN 232
DB 177 WYQQKPGQSPKLLIYGASTRESGVDRPTGSGSGTDFTLTISSVQASDLAVIYQNDHSY 236
QY 233 HWVFGGTGKTLVLPQKPSAAAGSQKLISERDLNSHHHHH 273
DB 237 PLTFGAGTKLEI-----KHHHHH 255
RESULT 10
Q9ETI3_MOUSE PRELIMINARY; PRT; 109 AA.
ID Q9ETI3_MOUSE PRELIMINARY; PRT; 109 AA.
AC Q9ETI3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Song M.-Y., Kang H.-K., Kwag W.-J., Moon H.-J., Song T.-H., Ko I.-Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF287275; AAG03053.1; -; mRNA.
DR HSSP; P01724; 1AGV.
DR SMR; Q9ETI3; 1-109.
DR Ensembl; ENSMUSG00000064012; Mus musculus.
```

```
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 11554 MW; 4F91E9D351B1E158 CRC64;
SQ
Query Match 36.6%; Score 538.5; DB 2; Length 109;
Best Local Similarity 92.7%; Pred. No. 4.3e-35;
Matches 102; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
QY 137 QAVVQESALTTPSPGTVTLTCSRNTGTTTNNYANWVQEKPDHLEFTGLIHTNNRAGV 196
DB 1 QAVVQESALTTPSPGTVTLTCSRSTGATTTNNFANWVQEKPDHLEFTGLIHTNNRPGV 60
QY 197 PARFSGSLIGDKAALTITGAQTEDEALYFCALWYNNHVVFGGTKTLTVLG 246
DB 61 PARFSGSLIGDKAALTITGAQTEDEALYFCALWYNN-VWFGGTKTLTVLG 109
RESULT 11
Q6SZC8_HUMAN PRELIMINARY; PRT; 244 AA.
ID Q6SZC8_HUMAN PRELIMINARY; PRT; 244 AA.
AC Q6SZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbr0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAA73500.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 244
FT SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
SQ
Query Match 36.3%; Score 533; DB 2; Length 244;
Best Local Similarity 46.6%; Pred. No. 3.2e-34;
Matches 118; Conservative 39; Mismatches 74; Indels 22; Gaps 6;
QY 3 QVQLQSGAEIARPGASVKMSCKASGYTFYTHHWVRQRPGLDLEWIGINPSSGYSY 62
DB 1 QVQLVQSGAEVKKPDSVKVKSCRAAGFTFSYDHYHWHWRQAPGQGLEWGWIDPNNGDRF 60
QY 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVYCYARR-----ADYGNIEYTWYAWQGG 118
DB 61 AQRFGQRTWTRDTSISAAAYEVSRLSDDTAVVYCARREGTGSIAIG-----MDVWQGG 114
QY 119 TTVTVSSAKTTPKLG-----DIQAVVQEP-SALTTPSPGTVTLTCSRNTGTTTNYA 171
DB 115 TLTVTVSGGGSGGGSGGGSDIQ--MTQSPFSLASIGDRVITTCRASEGIY---HWL 169
QY 172 NWVQEKPDHLEFTGLIHTNNRAGVPAPRPSGLIGDKAALTITGAQTEDEALYFCALWYNN 231
DB 170 AWYQQKPGKAPKFLIYKASSLASAPRSFSGSGSGTDFTLTISSLPDPPATYIYQQYSN 229
QY 232 NHWVFGGTKTLTV 244
```

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Db
||||| :
230 YPLTFGGGKLEI 242

RESULT 12
LV2B_MOUSE STANDARD; PRT; 129 AA.
AC P01729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda-2 chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82274221; PubMed=6287422;
RA Wu G.E., Govindji N., Hozumi N., Murialdo H.;
RT "Nucleotide sequence of a chromosomal rearranged lambda 2
Nucleic Acids Res. 10:3831-3843 (1982).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382 (1982).
[3]
RP NUCLEOTIDE SEQUENCE OF 1-22.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845 (1979).
[4]
RP PROTEIN SEQUENCE OF 20-129.
RX MEDLINE=74048693; PubMed=4760498;
RA Dugan E.S., Bradshaw R.A., Simms E.S., Eisen H.N.;
RT "Amino acid sequence of the light chain of a mouse myeloma protein
(MOPC-315).";
RL Biochemistry 12:5400-5416 (1973).
[5]
RP DETERMINATION OF AMIDATION STATES OF 58; 59; 62; 100; 102 AND 115.
RX MEDLINE=78187254; PubMed=418802;
RA Gavish M., Zakut R., Wilchek M., Givol D.;
RT "Preparation of a semisynthetic antibody.";
RL Biochemistry 17:1345-1351 (1978).
CC -!- MISCELLANEOUS: This chain is from a myeloma protein with anti-DNP
activity.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC PIR; A93431; L2MS35.
CC HSSP; P01724; 1A6V.
CC SMR; P01729; 20-129.
CC Ensembl; ENSMUSG00000064012; Mus musculus.
CC InterPro; IPR002197; HTH_Fis.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC PRINTS; PR01590; HTHFIS.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid; Signal.
KW SIGNAL 1 19
```

```
FT CHAIN 20 129 Ig lambda-2 chain V region MOPC 315.
FT DOMAIN 20 125 Ig-like.
FT MOD_RES 20 20 Pyrrolidone carboxylic acid.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13418 MW; 0AA6E8125723552C CRC64;

Query Match 35.4%; Score 520; DB 1; Length 129;
Best Local Similarity 85.1%; Pred. No. 1.6e-33;
Matches 97; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 133 GGGIQAQVTSALTSPTGVTTLTCRSNTGTVTTSNTYANWVQKPDHLFTGLIGTNNR 192
Db 16 GASSAAVVTQESALTSPTGVTTLTCRSSTGAVTTSYANWVQKPDHLFTGLIGTSNR 75
QY 193 APGVPARFSGSLIGDKAALITGATGDEAIYFCALWNNHNVFGGKLTVLG 246
Db 76 APGVPRFSGSLIGDKAALITGATGDEDDAMVFCALWFRNHFVFGGKTVTLG 129

RESULT 13
Q9D8L4_MOUSE PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:181006009 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
GN Name=Igh-la;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guskinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RT
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RL Nature 420:563-573 (2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RN Genome Res. 10:1617-1630 (2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RN Genome Res. 10:1757-1771 (2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN EMBL; AK007918; BAB25349.1; -; mRNA.  
DR PIR; PH1165; PH1165.  
DR PIR; S19966; S19966.  
DR PIR; S26746; S26746.  
DR HSP; P01864; IBOG.  
DR SWR; Q9DBL4; 20-469.  
DR Ensembl; ENSMUSG00000054328; Mus musculus.  
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DR GO; GO:0005771; C:multivesicular body; IDA.  
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DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.  
DR GO; GO:0003033; P:antigen processing; IDA.  
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.  
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.  
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.  
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.  
DR GO; GO:00050871; P:positive regulation of B cell activation; IDA.  
DR GO; GO:00050778; P:positive regulation of immune response; IDA.  
DR GO; GO:00050766; P:positive regulation of phagocytosis; IDA.  
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.  
DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.  
DR GO; GO:0003162; P:regulation of proteolysis and peptidolysis; IDA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003106; Ig MHC.  
DR InterPro; IPR003596; Ig v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
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SEQUENCE 617 AA; BCF2AEC857CD3D12 CRC64;  
  
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Best Local Similarity 45.0%; Pred. No. 4.3e-32;  
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SEQUENCE 617 AA; BCF2AEC857CD3D12 CRC64;  
  
Query Match 35.3%; Score 519.5; DB 2; Length 473;  
Best Local Similarity 58.6%; Pred. No. 8.5e-33;  
Matches 112; Conservative 20; Mismatches 40; Indels 19; Gaps 4;  
  
QY 3 QVQLQSGAELARPGASVKMSCKASGYTFTTYYTHWVRQRPGLHWIYINPSSGYSYD 62  
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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
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OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
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RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Teohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
RG NIH MGC Project;  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC098504; AAH98504.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;  
  
Query Match 34.9%; Score 512.5; DB 2; Length 617;  
Best Local Similarity 45.0%; Pred. No. 4.3e-32;  
Matches 126; Conservative 36; Mismatches 79; Indels 39; Gaps 10;

Db 19 SQVLOQSGAEALAKPGASVKLSCKASGYTFTSWMHVVKORPCQGLEWIGYNPSSGYTK 78  
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QY 122 TVSS-AKTPKLGDDIQAVVQESALTTPSGETVTLTCRSNTGTVTTSYANWVQKPDH 180  
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QY 181 LFTGLIGHTNNRAGVPARFSGSLIGDKAALITGAQTDEAIYFCALAYNNHNVFGGCT 240  
Db 191 VIQGIKTFPLTRGGKYLATSQVLLSPKSL-----EGSDEYL-VCKIHY-----GGKN 238  
QY 241 K-----LTVLGPK-----SAAAGSEQKLISE 262  
Db 239 KDLHVPPIPAVAENPNVNVFVPRDGFSGPAPRKSKLICE 278

RESULT 15

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DT 01-DEC-2001 (Tremblrel. 26, Last annotation update)  
DE Anti-CEA 79 single chain Fv (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98170165; PubMed=9509426;  
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
RT "Cloning and characterization of cDNAs encoding VH and VL of a  
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
RT generation of a single-chain Fv molecule (scfv).";  
RL Mol. Cells 7:816-819(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;  
RA Stark S.E., Caton A.J.;  
RA "Antibodies that are specific for a single amino acid interchange in a  
RT protein epitope use structurally distinct variable regions.";  
RL J. Exp. Med. 174:613-624(1991).  
DR EMBL; U88067; AAB48044.1; -; mRNA.  
DR PIR; S19965; S19965.  
DR PIR; S19967; S19967.  
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DR HSSP; P01607; 1BWV.  
DR Ensembl; ENSMUSG0000021155; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
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Job time : 167.882 secs



GenCore version 5.1.7  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/H COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037.5	70.6	402	1	US-08-491-988-9
2	1035.5	70.4	415	1	US-08-491-988-7
3	1035.5	70.4	435	1	US-08-491-988-5
4	1026.5	69.8	269	1	US-08-428-257A-72
5	1026.5	69.8	269	1	US-08-491-988-3
6	730	49.7	288	2	US-09-423-439-38
7	696	47.3	495	2	US-09-948-004-18
8	685	46.6	258	2	US-09-526-738A-4
9	678	46.1	239	2	US-08-279-772A-8
10	678	46.1	239	2	US-08-902-486-11
11	677	46.1	246	1	US-08-469-486-57
12	677	46.1	246	1	US-08-469-658-57
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18	650.5	44.3	673	2	US-09-423-439-32
19	648	44.1	270	2	US-09-976-118-2
20	644.5	43.8	264	2	US-10-114-716A-46
21	641.5	43.6	244	1	US-08-553-497A-22
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24	634	43.1	553	2	US-09-188-082-16
25	634	43.1	553	2	US-09-364-088-16
26	634	43.1	553	2	US-09-102-716-16
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30	631	42.9	240	2	US-09-296-595-8	Sequence 8, Appl
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33	618.5	42.1	244	2	US-09-940-391-1	Sequence 1, Appl
34	617.5	42.0	483	1	US-08-392-338A-19	Sequence 19, Appl
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36	617.5	42.0	483	2	US-09-166-093-19	Sequence 19, Appl
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38	617.5	42.0	483	2	US-09-166-094-19	Sequence 19, Appl
39	617.5	42.0	483	2	US-09-443-213-19	Sequence 19, Appl
40	614.5	41.8	271	1	US-08-894-922A-10	Sequence 10, Appl
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43	612.5	41.7	242	1	US-08-553-497A-28	Sequence 28, Appl
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45	607	41.3	637	1	US-08-465-473B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-491-988-9  
; Sequence 9, Application US/08491988  
; Patent No. 5973116  
; GENERAL INFORMATION:  
; APPLICANT: EPENETOS, AGAMENNON A.  
; APPLICANT: SPOONER, ROBERT A.  
; APPLICANT: DEONARAIN, MAHENDRA  
; TITLE OF INVENTION: Compounds for targeting  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP  
; STREET: 261 MADISON AVENUE  
; CITY: NEW YORK  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/491,988  
; FILING DATE: 18-DEC-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GOLDBERG, JULES E.  
; REGISTRATION NUMBER: 24,408  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-986-4090  
; TELEFAX: 212-818-9479  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 402 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-491-988-9

Query Match	70.6%	Score 1037.5	DB 1	Length 402
Best Local Similarity	78.1%	Pred. No. 4.6e-70		
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US-08-428-257A-72
; Sequence 72, Application US/08428257A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428.257A
; FILING DATE: 07/05/95
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-257A-72

Query Match 69.8%; Score 1026.5; DB 1; Length 269;
Best Local Similarity 79.6%; Pred. No. 1.9e-69;
Matches 199; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

QY 1 MAQVQLQSGAGELARPGASVKMSCKASGYTFYTHHWVRQPGHLEWIGVNPSSGYS 60
DB 21 MAQVQLQPGAGELVKGASVKLSCKASGYTFYTHHWVVKQRPGRGLEWIGRIDPNSGGT 80
QY 61 DYNQPFKGTTLTADKSNNTAYMQLNSLTSEDSAVVYCARADYGNVEYTWFAWYQGQTT 120
DB 81 KNEKFKSKATLVDPKSTATMQLSSLTSEDSAVVYCAR---YDYGSSYFDYWGQTT 137
QY 121 VTVSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWVQE 176
DB 138 VTVSSGGSGGGSGGGGSAVVQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQE 197
QY 177 KPDLFTGLIGNNRPAGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 236
DB 198 KPDLFTGLIGTNNRPAGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 257
QY 237 GGGTKLTVLG 246
DB 258 GGGTKLTVLG 267

RESULT 5
US-08-491-988-3
; Sequence 3, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA

US-08-428-257A-72
; Sequence 72, Application US/08428257A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428.257A
; FILING DATE: 07/05/95
; CLASSIFICATION: 514
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-428-257A-72

Query Match 69.8%; Score 1026.5; DB 1; Length 269;
Best Local Similarity 79.6%; Pred. No. 1.9e-69;
Matches 199; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

QY 1 MAQVQLQSGAGELARPGASVKMSCKASGYTFYTHHWVRQPGHLEWIGVNPSSGYS 60
DB 21 MAQVQLQPGAGELVKGASVKLSCKASGYTFYTHHWVVKQRPGRGLEWIGRIDPNSGGT 80
QY 61 DYNQPFKGTTLTADKSNNTAYMQLNSLTSEDSAVVYCARADYGNVEYTWFAWYQGQTT 120
DB 81 KNEKFKSKATLVDPKSTATMQLSSLTSEDSAVVYCAR---YDYGSSYFDYWGQTT 137
QY 121 VTVSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWVQE 176
DB 138 VTVSSGGSGGGSGGGGSAVVQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQE 197
QY 177 KPDLFTGLIGNNRPAGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 236
DB 198 KPDLFTGLIGTNNRPAGVPARFSGSLIGDKAALTTGAQTEDEAIYFCALWYNNHWVF 257
QY 237 GGGTKLTVLG 246
DB 258 GGGTKLTVLG 267

RESULT 5
US-08-491-988-3
; Sequence 3, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMENNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA

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;
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB98/01294
;   FILING DATE: 05-MAY-1998
;   APPLICATION NUMBER: GB 9709421.3
;   FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 38:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 288 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;   MOLECULE TYPE: protein
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match      49.7%; Score 730; DB 2; Length 288;
Best Local Similarity 56.2%; Pred. No. 3.4e-47;
Matches 158; Conservative 24; Mismatches 77; Indels 22; Gaps 7;

QY 1 MAQVLOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 60
Db 21 MAQVLOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 80
QY 61 DYNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGTT 120
Db 81 DYNQNFKNKAITLVDSSTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGTT 138
QY 121 VTSSAKTTPKLG-----DIQAVVTQBSALTPSGETVTLTCRSNTGTV---TTSNYA 171
Db 139 VTSSGGGGGGGGGGGGGSDIE--LSQSPSLAVSAGEKVTWMSCKSSQSILNSRTRKNYL 197
QY 172 NWQEPDHLFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYN 231
Db 198 AMYQRPQSGPKLLIYWASTRTSGVDPDFTGSGGTDFTLTISVQAEDLAIYCKQSYT 257
QY 232 NHWVFGGKTKLTVLGQPKSAAGSEOKLISEEDLNSHHHH 272
Db 258 LR-TFGGGTKLEI-----KREQKLISEEDLNHHHHH 288

RESULT 7
US-09-948-004-18
; Sequence 18, Application US/09948004
; Patent No. 672358
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
;   immunological disorders
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948, 004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18

Query Match      47.3%; Score 696; DB 2; Length 495;
Best Local Similarity 51.2%; Pred. No. 2.3e-44;
Matches 147; Conservative 29; Mismatches 59; Indels 52; Gaps 7;

QY 2 AOVLQOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 61
Db 246 SDIKLQOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 305
QY 62 YNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGTTV 121
Db 306 YNQNFKDKATLTADKSSNTAYMQLNSLTSEDSAVYVCARYD---DHYCLDYWRQGTTL 361
QY 122 TVSSAKTTPKLG-----DIQAVVTQBSA-LTTPSGETVTLTCRSNTGTV 166
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;
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB98/01294
;   FILING DATE: 05-MAY-1998
;   APPLICATION NUMBER: GB 9709421.3
;   FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 38:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 288 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;   MOLECULE TYPE: protein
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match      46.6%; Score 685; DB 2; Length 258;
Best Local Similarity 56.1%; Pred. No. 7.1e-44;
Matches 147; Conservative 32; Mismatches 59; Indels 24; Gaps 6;

QY 1 MAQVLOQSGAELARPGASVMSCKASGYFTFTYTHWVRQPHDLEWIGYNPSSGYS 60
Db 1 MAQVLOQSGAELARPGASVMSCKASGYFTFTSYMWNVVKQRPQGQLEWIGYNPTGT 60
QY 61 DYNQNFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYVCARRADYGNVEYTWFAWYQGTT 120
Db 61 KYNQFKDKATLTADKSSNTAYMQLNSLTINVDNAVYCTT-----GYSYFDYWGQGT 113
QY 121 VTSSAKTTPKLG-----DIQAVVTQBSA-LTTPSGETVTLTCRSNTGTVTSNYANW 173
Db 114 VTSSGGGGGGGGGGGGGSDIE--LTQSPAIMSASPGKVTITCSASSV---NYMHW 167
QY 174 VOEKPDLHFTGLIGHTNNRAGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYNNH 233
Db 168 FOQKPGTSPKLIWISSTNSNLASGVPARFSGSGSGTSLTISRMEADAATYYCQQRSSYP 227
QY 234 WYVFGGKTKLTVLGQPKSAAGS 255
Db 228 YTFGGGKTL-----QIKRAAAGA 245

RESULT 9
US-08-279-772A-8
; Sequence 8, Application US/08279772A
; Patent No. 6080560
; GENERAL INFORMATION:
; APPLICANT: Russell, David R
; APPLICANT: Fuller, James T
; TITLE OF INVENTION: Method for Producing Antibodies in Plant
;   Cells
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Quarles and Brady
;   STREET: PO Box 2113
;   CITY: Madison
;   STATE: WI
;   COUNTRY: United States of America
;   ZIP: 53701-2113
```



```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-57

Query Match          46.1%; Score 677; DB 1; Length 246;
Best Local Similarity 55.1%; Pred. No. 2.7e-43;
Matches 146; Conservative 29; Mismatches 70; Indels 20; Gaps 6;

QY 3 QVLOQSGAELARPGASVKMSCKASGYTFYTHWVROPGRHDLIEWIGYINPSSGYSY 62
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 1 QVQLQSGAELVKPGASVKMSCKASGYTFASYWINVWKORPGQGLEWIGHIYIPVRSITKY 60
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 63 NQPFKKTTLTADKSNNTAYMQLNSLTSDSAVYYCARRADYGNVEYTFWYWGQGTITVT 122
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 61 NEKFKSKATLTLDTSSTAYMQLSSLTSDSAVYYCSRG---DGSYYAMDYWGQGTITVT 117
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 123 VSSAKTTPKLGDIQAVVTQESA-LTTSPTGETVTLTCRNTGTVTTSNYANWVQEKPDHL 181
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 118 VSSG-----GGSDIELTQSPAILSPGKVTMTCRASSV---STHWYQQKPGSS 167
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 182 FTGLIGHTNNRPGVPAREPSGLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGK 241
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 168 PKWIVATSNLGSVPTRFSGTSGTSYSLTISRVEADAATYYCQWSENRPFTFGSGTK 227
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 242 LTVLGQPKSAAAGSEQKLISEEDLN 266
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 228 LEI-----KRAAA--EQKLISEEDLN 246
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

```
RESULT 12
US-08-469-658-57
; Sequence 57, Application US/08469658
; Patent No. 5917018
; GENERAL INFORMATION:
; APPLICANT: Th egersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
```

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;
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-658-57

Query Match          46.1%; Score 677; DB 1; Length 246;
Best Local Similarity 55.1%; Pred. No. 2.7e-43;
Matches 146; Conservative 29; Mismatches 70; Indels 20; Gaps 6;

QY 3 QVLOQSGAELARPGASVKMSCKASGYTFYTHWVROPGRHDLIEWIGYINPSSGYSY 62
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 1 QVQLQSGAELVKPGASVKMSCKASGYTFASYWINVWKORPGQGLEWIGHIYIPVRSITKY 60
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 63 NQPFKKTTLTADKSNNTAYMQLNSLTSDSAVYYCARRADYGNVEYTFWYWGQGTITVT 122
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 61 NEKFKSKATLTLDTSSTAYMQLSSLTSDSAVYYCSRG---DGSYYAMDYWGQGTITVT 117
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 123 VSSAKTTPKLGDIQAVVTQESA-LTTSPTGETVTLTCRNTGTVTTSNYANWVQEKPDHL 181
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 118 VSSG-----GGSDIELTQSPAILSPGKVTMTCRASSV---SYHWYQQKPGSS 167
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 182 FTGLIGHTNNRPGVPAREPSGLIGDKAALTITGAQTEDEAIYFCALWYNNHWVFGGK 241
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 168 PKWIVATSNLGSVPTRFSGTSGTSYSLTISRVEADAATYYCQWSENRPFTFGSGTK 227
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 242 LTVLGQPKSAAAGSEQKLISEEDLN 266
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 228 LEI-----KRAAA--EQKLISEEDLN 246
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

```
RESULT 13
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Huananus
; US-09-526-738A-2

Query Match          46.0%; Score 676; DB 2; Length 256;
Best Local Similarity 55.8%; Pred. No. 3.3e-43;
Matches 145; Conservative 32; Mismatches 59; Indels 24; Gaps 6;

QY 3 QVLOQSGAELARPGASVKMSCKASGYTFYTHWVROPGRHDLIEWIGYINPSSGYSY 62
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 1 QVQLQSGAELAKPGASVKMSCKTSGYTFYSYMMNVWKORPGQGLEWIGYINPTTGYTKY 60
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
QY 63 NQPFKKTTLTADKSNNTAYMQLNSLTSDSAVYYCARRADYGNVEYTFWYWGQGTITVT 122
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 61 NQPFKDKATLTADKSSSTAYMQLSSLTNTVDSAVYYCTT-----GYSYFDYWGQGTITVT 113
   ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
```

Qy	123	VSSAKTTPKLG-----DIQAVVTQESA-LTTSPGETVLTCSRNTGTVTTSNYANWQ	175
		:    :    :    :    :    :    :    :    :    :    :    :	
Db	114	VSSGGSGGGSGGGGGDIE--LTSIPAISAPGEKVITTCSSASV---NYMHWFQ	167
Qy	176	EYEDHLFTCLIGHTNNRAGVPARESGSLIGDKAALITTCGAOTDEAIYFCALWYNHHV	235
		:    :    :    :    :    :    :    :    :    :    :    :    :	
Db	168	QPGTSPKLWISSTNLASGPAREFSGSGTSLIIRMEADAATYYICQORSSYPYT	227
Qy	236	FGGGTKLVLGQPKSAAAGS	255
Db	228	FGGGTKL-----OIKDAAGA	243

RESULT 14  
US-08-463-163-3  
Sequence 3, Application US/084631163  
Patent No. 5696237  
GENERAL INFORMATION:  
APPLICANT: FitzGerald, David J.  
APPLICANT: Chaudhary, Vijay K.  
APPLICANT: Pastan, Ira H.  
APPLICANT: Waldmann, Thomas A.  
APPLICANT: Queen, Cary L.  
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Crew  
STREET: One Market Plaza, Steuart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

Query Match 45.9%; Score 675; DB 1; Length 599;  
Best Local Similarity 53.9%; Pred. NO. 1.1e-42;  
Matches 146; Conservative 31; Mismatches 78; Indels 16; Gaps 4;

```

QY 3 QVQLQSGAEIARPGASVKMSCKASGYTFTYTIHWVQRPGLHLEWIGYNPSSGYSYDY 122
DB 2 QVQLQSGAEIARPGASVKMSCKASGYTFTSYRMHWVKQRPQGLEWIGYNPSTGYTEY 61
QY 63 NONPKGKTLTADKSSNTAYMQLNSLTSEDSAVVYCCARRADYGNVEYTWTFAYWGQGTITV 122
DB 62 NQPKPKATLTADKSSNTAYMQLNSLTSEDSAVVYCCARRADYGNVEYTWTFAYWGQGTITV 114
QY 123 VSS-----AKTTPKLGDDIQAIVVQESA-LTTSPGETVTLTCSRNTGTVTTSNYANWVQEK 177
DB 115 VSSGGGSGGGSGGGSGGQIVLVLTQSPAIMSASPGKVTITCSAS-----SSISYMHWFQOK 170
QY 178 PDHLFTGLCHTNRRAPGVPARSGSLIGKAAITITGAQTEDEAIVFCALWYNNHWFVG 237
DB 171 PGTSPLKIYITNSLASGVPARFSGSGSYSLTISRMEAEAAATYYCHORSTYPLPTFG 230
QY 238 GGTKLTIVLGQPKAAAGSEQKLISEEDLNH 268
DB 231 SGTKLELKGSLAALTAHQACHLPLETFTH 261

RESULT 15
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids

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GenCore version 5.1.7  
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# OM protein - protein search, using sw model

Run on: February 9, 2006, 03:53:23 ; Search time 127.57 Seconds  
(without alignments)

894.155 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQSGAELARPGASV.....GSEQLISBEDLNSHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	709	48.2	492	4	US-10-682-845-81
2	707	48.1	492	4	US-10-682-845-63
3	707	48.1	492	4	US-10-682-845-73
4	707	48.1	492	4	US-10-682-845-85
5	706	48.0	492	4	US-10-682-845-61
6	705	48.0	492	4	US-10-682-845-71
7	704	47.9	492	4	US-10-362-591-2
8	704	47.9	492	4	US-10-682-845-59
9	704	47.9	492	4	US-10-682-845-75
10	704	47.9	492	4	US-10-682-845-87
11	704	47.9	500	4	US-10-168-809-22
12	703	47.8	492	4	US-10-682-845-83
13	702	47.8	492	4	US-10-682-845-67
14	701	47.7	492	4	US-10-682-845-65
15	701	47.7	492	4	US-10-682-845-79
16	700.5	47.7	243	5	US-10-879-994-10
17	700.5	47.7	243	5	US-10-610-452-10
18	700	47.6	295	4	US-10-406-830-7
19	700	47.6	492	4	US-10-682-845-77
20	699	47.6	492	4	US-10-682-845-69
21	696	47.3	495	3	US-09-948-004-18
22	696	47.3	495	5	US-10-672-932-18
23	686	46.7	260	4	US-10-435-614-20
24	684	46.6	258	4	US-10-247-488-4
25	684	46.5	260	4	US-10-435-614-19
26	683.5	46.5	249	3	US-09-880-748-1838
27	683.5	46.5	249	4	US-10-293-418-1838

Sequence 6, Appli  
Sequence 88, Appl  
Sequence 111, App  
Sequence 1523, Ap  
Sequence 1523, Ap  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 113, App  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 48, Appli  
Sequence 48, Appl  
Sequence 45, Appl  
Sequence 102, App  
Sequence 45, Appl  
Sequence 59, Appl  
Sequence 14, Appl

28 681 46.3 291 4 US-10-406-830-6  
29 679.5 46.2 438 4 US-10-244-821-88  
30 677 46.1 499 5 US-10-805-177-111  
31 676.5 46.0 245 3 US-09-880-748-1523  
32 676.5 46.0 245 4 US-10-293-418-1523  
33 676 46.0 243 5 US-10-866-406-2  
34 676 46.0 256 4 US-10-247-488-2  
35 674.5 45.9 524 5 US-10-805-177-113  
36 673 45.8 423 4 US/10/150  
37 673 45.8 423 4 US/10/150  
38 673 45.8 423 4 US/10/244  
39 672.5 45.7 657 5 US-10-723-003-48  
40 672.5 45.7 657 6 US-11-004-639-48  
41 672 45.7 145 4 US-10-365-123-45  
42 671 45.6 291 6 US-11-093-103-102  
43 670 45.6 243 5 US-10-966-406-45  
44 669.5 45.5 258 4 US-10-239-656-59  
45 667 45.4 248 5 US-10-879-994-14

## ALIGNMENTS

### RESULT 1

US-10-682-845-81  
; Sequence 81, Application US/10682845  
; Publication No. US20040162411A1  
; GENERAL INFORMATION:  
; APPLICANT: Lanzavecchia, Antonio  
; TITLE OF INVENTION: Potent T cell modulating molecules  
; FILE REFERENCE: G2296 US  
; CURRENT APPLICATION NUMBER: US/10/682,845  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: US 60/419,149  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: CA 2,403,313  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 81  
; LENGTH: 492  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: scFv EpCAMxCD3 with M58 mutant in anti-CD3 part  
US-10-682-845-81

Query Match 48.2%; Score 709; DB 4; Length 492;  
Best Local Similarity 51.9%; Pred. No. 8e-42;  
Matches 149; Conservative 28; Mismatches 58; Indels 52; Gaps 7;

Qy 2 AQVQLQSGAELARPGASVKMSCKASGYTFTYTIHWVRPQGHDLWVGNPSSGYSD 61  
Db 243 SDIKLQSGAELARPGASVKMSCKTSGYFTYTIHWVRPQGHDLWVGNPSSGYSD 302  
Qy 62 YNQNFKGKTTLTADKSNATYMLNLSLSDSAVYVCARRADYGNVEYTFYAYGQGTIV 121  
Db 303 YNQKFKDKALITTDKSSSTAYMLNLSLSDSAVYVCARRADYGNVEYTFYAYGQGTIV 358  
Qy 122 TVSSAKTTPKLG-----DIQAVTQESA-LTTSFGETVTLTCRNTGVT 166  
Db 359 TVSSVE-----GGSGGGGGGGVDDIQ--LTQSPAINASASPGKVTMTCRASSSV-- 409  
Qy 167 TSNYANVQKPDHFLTGLTGHNTNRPAGVPARESGSLIGDKAALTITGAQTEDEAIYFC 226  
Db 410 --SYNNYQKSGTSPKRWIYDTSKVASGVPYRFSGSGSGTSTLTSSMEADAATYYC 467  
Qy 227 ALVYNNHWFGGKTLTVLQPKSAAGSEKLISEEDLNSHHHHH 273  
Db 468 QQWSSNPLTFGAGTKLEL-----KHHHHH 492

### RESULT 2



Query Match	48.0%;	Score 705;	DB 4;	Length 492;				
Best Local Similarity	52.3%;	Pred. No. 1.5e-41;						
Matches 150;	Conservative 27;	Mismatches 58;	Indels 52;	Gaps 8;				
2	AQVLOQSGAE	LARPGASV	KMSCKASGY	FTTYYTTHV	RQPHDLEW	IGHINPSSG	YSYD 61	
2y	:	:	:	:	:	:	:	
243	SDIKQOQSGAE	LARPGASV	KMSCKTSGY	FTTYYTTHV	RQPHDLEW	IGHINPSSG	YSYD 302	
2y	:	:	:	:	:	:	:	
62	YNQNFPGKTT	LTDKSSNTAY	QMLNSLTSED	SAVYCCARRADY	GYNYETW	FAYMQQGTV	121	
2y	:	:	:	:	:	:	:	
303	YNQKFFDKAT	LTTDKSSSTAY	QMLNSLTSED	SAVYCCAR	--YFNDHYC	-LDYMQQGTTL	358	
2y	:	:	:	:	:	:	:	
122	TVSSAKTTP	PKLGG	-----	DIQAVVTOESA	-LTSPOET	TTLCSRNTGYT	166	
2y	:	:	:	:	:	:	:	
359	TVSSVE	-----	CGSGSGSGSGSGG	VDDIQ--	LTPSPAIMS	ASPGKVTMT	CRASSV-- 409	
2y	:	:	:	:	:	:	:	
167	TSNYANVNVQ	EKPDH	LFTGL	IHTNNRAP	GVPARFSGSL	IGDKAAL	TTGAOTED	EAIYFC 226
2y	:	:	:	:	:	:	:	
410	--STNNVYQ	QSGTS	PKRWI	YDTSKVAS	GVPRFSGSG	SGTSYSL	TISSMEAR	EADAATYVC 467
2y	:	:	:	:	:	:	:	
227	ALWYNNHWF	GGGT	KTLVT	LQPKSA	AAGSEQ	KLISEED	LNSHHHH	273
2y	:	:	:	:	:	:	:	
468	QOKSSNP	PLTF	GAGTK	LEL	-----	KHHHH	492	
2y	:	:	:	:	:	:	:	

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RESULT 7
US-10-362-591-2
; Sequence 2, Application US/10362591
; Publication No. US20040072749A1
; GENERAL INFORMATION:
; APPLICANT: ZOCHER, MARCEL
; APPLICANT: BAUERLE, PATRICK
; APPLICANT: DREIER, TORSTEN
; TITLE OF INVENTION: COMPOSITION FOR THE ELIMINATION OF AUTOREACTIVE B-CELLS
; FILE REFERENCE: 029976-0110
; CURRENT APPLICATION NUMBER: US/10/362,591
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09714
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: EP 00117354.1
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-591-2

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[illegible]





Db 410 --SYNNWYQOKSGTSPKRWIYDTSKVASGVYRFGSGSGTYSLTITSSAEADAATTC 467  
227 ALWYNNHWYFGGKTKTVLQPKPSAAAGSEBQLISEEDLNSHHHHH 273  
Db 468 QOWSSNPLTFGAGTKLEL-----KHHHHH 492

Query Match 47.1%; Score 70.1; DB #; Mengen 432;  
Best Local Similarity 51.6%; Pred. No. 2.9e-41;  
Matches 148; Conservative 28; Mismatches 59; Indels 52; Gaps 7;

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RESULT 14
US-10-682-845-65
; Sequence 65, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 452
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAmxCD3 with M7 mutant in anti-CD3 part
US-10-682-845-65

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```

RESULT 15
US-10-682-845-79
; Sequence 79, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOURCE: Patent in version 3.1

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2006, 03:55:47 ; Search time 19.9009 Seconds  
(without alignments)  
180.014 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQQSGAELARPGASV.....GSRQLISBEDLNHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	683.5	46.5	249	7	US-11-054-515-1838
2	676.5	46.0	245	7	US-11-054-515-1523
3	674	45.9	615	6	US-10-512-184-50
4	668.5	45.5	290	7	US-11-032-773-957
5	660.5	44.9	245	7	US-11-054-515-1919
6	659	44.8	319	7	US-11-032-773-955
7	654	44.5	250	7	US-11-054-515-1722
8	651.5	44.3	247	7	US-11-054-515-948
9	651	44.3	248	7	US-11-054-515-1643
10	651	44.3	250	7	US-11-054-515-1723
11	650.5	44.3	247	7	US-11-054-515-927
12	649	44.1	248	7	US-11-054-515-893
13	647	44.0	248	7	US-11-054-515-1681
14	646.5	44.0	251	7	US-11-054-515-1496
15	646	43.9	254	7	US-11-054-515-2082
16	644.5	43.8	251	7	US-11-054-515-1688
17	644	43.8	248	7	US-11-054-515-1609
18	643.5	43.8	251	7	US-11-054-515-1459
19	643	43.7	248	7	US-11-054-515-1679
20	642.5	43.7	253	7	US-11-054-515-1936
21	640.5	43.6	243	7	US-11-054-515-1959
22	640	43.5	248	7	US-11-054-515-1622
23	639	43.5	248	7	US-11-054-515-1660
24	639	43.5	248	7	US-11-054-515-1670
25	639	43.5	248	7	US-11-054-515-1755

26	638.5	43.4	249	7	US-11-054-515-1753	Sequence 1753, Ap
27	637.5	43.4	249	7	US-11-054-515-1299	Sequence 1299, Ap
28	637.5	43.4	255	7	US-11-054-515-1156	Sequence 1156, Ap
29	637	43.3	248	7	US-11-054-515-950	Sequence 950, App
30	637	43.3	248	7	US-11-054-515-953	Sequence 953, App
31	637	43.3	248	7	US-11-054-515-1181	Sequence 1181, Ap
32	637	43.3	248	7	US-11-054-515-1623	Sequence 1623, Ap
33	636.5	43.3	249	7	US-11-054-515-1290	Sequence 1290, Ap
34	636	43.3	248	7	US-11-054-515-900	Sequence 900, App
35	636	43.3	248	7	US-11-054-515-980	Sequence 980, App
36	636	43.3	248	7	US-11-054-515-1293	Sequence 1293, Ap
37	636	43.3	248	7	US-11-054-515-1721	Sequence 1721, Ap
38	636	43.3	250	7	US-11-054-515-1647	Sequence 1647, Ap
39	635.5	43.2	241	7	US-11-054-515-2031	Sequence 2031, Ap
40	635.5	43.2	251	7	US-11-054-515-1077	Sequence 1077, Ap
41	635	43.2	242	7	US-11-054-515-2106	Sequence 2106, Ap
42	635	43.2	246	7	US-11-054-515-1192	Sequence 1192, Ap
43	635	43.2	252	7	US-11-054-515-1462	Sequence 1462, Ap
44	635	43.2	254	7	US-11-054-515-1699	Sequence 1699, Ap
45	635	43.2	256	7	US-11-054-515-1699	Sequence 1621, Ap

#### ALIGNMENTS

##### RESULT 1

US-11-054-515-1838  
; Sequence 1838, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1838

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-1838

Query Match 46.5%; Score 683.5; DB 7; Length 249;

Best Local Similarity 55.6%; Pred. No. 2.7e-37;

Matches 139; Conservative 32; Mismatches 72; Indels 7; Gaps 3;

Qy 3 QVQLQQSGAELARPGASVQMSCKASGYTFYTHVRQRPGHDLIEWIGINPSSGSDY 62

Db 1 QVQLQQSGAELARPGASVQMSCKASGYTFYTHVRQRPGHDLIEWIGINPSSGSDY 60

Qy 63 QNPFKGTTLTADKSSNTAYMQLNSLTSEDASVYCCARRADYNYEYTWFAWGQGTVT 122

Db 61 AERLQGRVITITADELTRVTVMELSSLRSEDTAVVYCARESEGGDYTNP-FGYWGRGTTVT 119  
Qy 123 VS-----SAKTPKLGDDQAVVTOESALTTSPGETVTLTCRNTGTVTTSYANVWQEK 177  
Db 120 VSSGGGGGGGGGGGSAQAVVIOBPSLTVSPGTVTLTCTSTGAVTNNNYPSWFOOK 179  
Qy 178 PDLHFTGLIGHTNNRAGVPARFSGSLIGDKAALTTTGATQDEAIYFCALWYNN-HWVF 236  
Db 180 PGAPRPLISWNNRSPWTPARFSAYLLGGKAVLTLGSGVQPEDEABEYCLLYSGDQQLVF 239  
Qy 237 GGGTKLTVLG 246  
Db 240 GGGKTVLG 249

## RESULT 2

US-11-054-515-1523  
; Sequence 1523, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1523  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1523

Query Match 46.0%; Score 676.5; DB 7; Length 245;  
Best Local Similarity 56.8%; Pred. No. 7.3e-37;  
Matches 142; Conservative 27; Mismatches 69; Indels 13; Gaps 4;  
Qy 3 QVQLQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLWIGYINPSSGYSY 62  
Db 1 QVQLVSGAEVKPGSVKVKCKASGTVSSRTISNVRQAPGQGLEWMGSLPPSGAPIY 60  
Qy 63 NQMFKGTTLTADKSSNTAYMQLNSLTSEDSAVVYCARRADYGNBYETWFAYWQGT 122  
Db 61 AQKQGRVAITADALTNTAFMELSLKSDDTAVVYCAR--DQGRY----LDLWKGKTLVT 114  
Qy 123 VS-----SAKTPKLGDDQAVVTOESALTTSPGETVTLTCRNTGTVTTSYANVWQEK 177  
Db 115 VSSGGGGGGGGGGGSAQVVIQPSLTVSPGTVTLTCSITGAVTSGNTPNFWFOOK 174  
Qy 178 PDLHFTGLIGHTNNRAGVPARFSGSLIGDKAALTTTGATQDEAIYFCALWYNN--NHWV 235  
Db 175 PGAPRALIYSTDNKHSWTPARFSGSLIGDKAALTLGSGVQPEDEADYCLLYGGAPWV 234

Qy 236 FGGGTKLTVLG 246  
Db 235 FGGGKTVLG 245

## RESULT 3

US-10-512-184-50  
; Sequence 50, Application US/10512184  
; Publication No. US20050244901A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.  
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
; TITLE OF INVENTION: resistance against fungi  
; FILE REFERENCE: 3581.01US01  
; CURRENT APPLICATION NUMBER: US/10/512,184  
; CURRENT FILING DATE: 2004-10-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker  
; OTHER INFORMATION: - scFv SS2 - cmcy/His6.  
US-10-512-184-50

Query Match 45.9%; Score 674; DB 6; Length 615;  
Best Local Similarity 51.9%; Pred. No. 2.3e-36;  
Matches 148; Conservative 33; Mismatches 80; Indels 24; Gaps 8;  
Qy 1 MAQVQLQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLWIGYINPSSGYS 60  
Db 342 MAQVQLQSGGTVLARPASVKMSCKASGYTFYTHHWVRQPGHDLWIGYINPSSGYS 401  
Qy 61 DYNQFPGKTTLTADKSSNTAYMQLNSLTSEDSAVVYCARRADYGNBYETWFAYWQGT 120  
Db 402 SYNQFPGKAKLTAVTSTSTAYMQLNSLTSEDSAVVYCTRT---DWDYA-MDYWGQGY 456  
Qy 121 VTVSSAKTT-----PKLG---GDIQAVVTOESA-LTTSPPGETVTLTCRNTGTVTTSY 170  
Db 457 VTVSSGTSVSGSKPGEGESTKGAPDIVLFQSPVMSASPGKVTWTCASSSV---NY 512  
Qy 171 ANWVQEKPDHFTGLIGHTNNRAGVPARFSGSLIGDKAALTTTGATQDEAIYFCALWY 230  
Db 513 IVWYQWKSQTSKRWIFDTSKLASGVVRFSGSGSGTSPSLTSSMEADIAITYCQWS 572  
Qy 231 NNHWVFGGTKLTVLGQPKSAAAGSEOKLISEDLNS--HHHHH 273  
Db 573 SPPLTFGAGTKLEL---KRAVDAAAQOKLISEDLGALDHHHHH 614

## RESULT 4

US-11-032-773-957  
; Sequence 957, Application US/11032773  
; Publication No. US20060018911A1  
; GENERAL INFORMATION:  
; APPLICANT: Ault-Riche, Dana  
; APPLICANT: Levy, Ronald  
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS  
; FILE REFERENCE: 17102-013001 / 1762  
; CURRENT APPLICATION NUMBER: US/11/032,773  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 60/536,184  
; PRIOR FILING DATE: 2004-01-12  
; PRIOR APPLICATION NUMBER: 60/557,591  
; PRIOR FILING DATE: 2004-03-29  
; NUMBER OF SEQ ID NOS: 958  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 957  
; LENGTH: 290



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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD S1C5 V5 His protein sequence
US-11-032-773-957

Query Match 45.5%; Score 668.5; DB 7; Length 290;
Best Local Similarity 50.0%; Pred. No. 2.7e-36;
Matches 147; Conservative 38; Mismatches 84; Indels 25; Gaps 7;

QY 1 MAQVQLQSGAEELARPGASVQMSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGSDY 60
DB 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGSDY 60
QY 63 NQNFPGKTTLTADKSSNTAYMQLNSLTSEDSAVYYCARRADYGNVEYTFWFAWVGQTT 122
DB 61 AQKFGQGRVTMTTRDTSTSTVMELSSLRSEDTAVYYCARDLS--GSYFSRYFDYWGQGLT 119
QY 123 VSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCSRNTGVTTSNYANWVQEKPD 179
DB 120 VSSGGSGGGSGGGSGGGSSSELTQDPAVSVLGGTVRIITCQ---GDSLRSYYASWYQQKPG 176
QY 180 HLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYN-----NH 233
DB 177 QAPVLVIYKNNRPPGIPDRFSGSSSGNTASLTITGAQAEADRYC-----NSRDSSGNH 232
QY 234 WVFEGGCTKLTVLG 246
DB 233 VVFEGGCTKLTVLG 245

RESULT 6
US-11-032-773-955
; Sequence 955, Application US/11032773
; Publication No. US20060018911A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032, 773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBAD S1C5 CD20 His Protein Sequence
US-11-032-773-955

Query Match 44.8%; Score 659; DB 7; Length 319;
Best Local Similarity 45.8%; Pred. No. 1.2e-35;
Matches 148; Conservative 38; Mismatches 83; Indels 54; Gaps 7

QY 1 MAQVQLQSGAEELARPGASVQMSCKASGYTFYTHHWVRQPGHDLIEWIGYNPSSGSDY 60
DB 1 MAEVQLQSGAEELVKKPGASVKISCKASGYTFTHDVIHWVKQRPEQGLEWIGTSPGNGDI 60
QY 61 DYNQNFPGKTTLTADKSSNTAYMQLNSLTSEDSAVYYCARRADYGNVEYTFWFAWVGQTT 120
DB 61 RYNEKFKDKATLTADKSSSTAYMQLNSLTSEDSAVYFCRISFY--YDNDYGDYWGQGT 118
QY 121 VTVSSAKTT-----PKLGGDIQAVVTQESA-LTTPGETVTLTCSRNTGVTTSNYA 171
DB 119 LTVSSSGAPGGGGGGGGGGSDIVLTQSPAIMSASLEERVMTCTASSS--VSSSYF 176
QY 172 NWQEKPDHLFTGLIGHTNNRAPGVPARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYN 231
DB 177 HWYQKPGSPKLIWYTTNSLGSVPARFSGSGGTSYSLTISSEAEADAATYCHQYHR 236
QY 232 NHWVFGGCTKLTVL-----GQPKSAAAGSEQKL-----ISEEDLN----- 266
DB 237 SPLTFGAGTKLELKRADAAPTVAASAASFLKISHFLKMSLNFTRAHTPYININCEPANP 296
QY 267 -----SHHHHH 273
DB 297 SEKNPSPTQCYNSAVDHHHHH 319

Query Match 44.9%; Score 660.5; DB 7; Length 245;
Best Local Similarity 54.5%; Pred. No. 7.6e-36;
Matches 138; Conservative 34; Mismatches 64; Indels 17; Gaps 5;

; TYPE: PRT
; ORGANISM: Homo sapiens
; TYPE: PRT
; LENGTH: 245
US-11-054-515-1919

Query Match 44.9%; Score 660.5; DB 7; Length 245;
Best Local Similarity 54.5%; Pred. No. 7.6e-36;
Matches 138; Conservative 34; Mismatches 64; Indels 17; Gaps 5;

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RESULT 7
US-11-054-515-1722
; Sequence 1722, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1722
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: Site
; LOCATION: (227)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-054-515-1722

Query Match 44.5%; Score 654; DB 7; Length 250;
Best Local Similarity 53.3%; Pred. No. 2e-35;
Matches 137; Conservative 35; Mismatches 65; Indels 20; Gaps 5;

QY 3 QVQLQSGAELARPGASVKMSCKASGYTFTTTHHWVRQPGHDLHWIGYINPSSGYSDY 62
DB 1 QVQLQSGAEVKPKGASVKSCASGYTFTGYTHWVRQAPGQGLEWMGWINENSGGTNY 60
QY 63 NQPFKGTTLTADKSNATYMWLNLSLTSDSAVYYCARRADY----GNYEYTFAYWGQ 118
DB 61 AQKFGQRTVMTSDTSSTAYMELSLRSDDTAVYCARVLPHVDILTGYSQNWFDPWGRG 120
QY 119 TTVTVSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWQ 175
DB 121 TLTVSSGGSGGGSGGGSSSELQDPAVSVALGQTVRITCQ---GDSLRSYYASWQ 177
QY 176 EKPDPHLFTGLHTNNRPAQVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYN---- 231
DB 178 QKPGQAPVLVIYGNKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC-----NSRDS 233
QY 232 --NHVFGGQTKLTVLG 246
DB 234 SGNHVFGGQTKLTVLG 250

RESULT 8
US-11-054-515-948
; Sequence 948, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
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; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 948
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: Site
; LOCATION: (227)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-054-515-948

Query Match 44.3%; Score 651.5; DB 7; Length 247;
Best Local Similarity 54.3%; Pred. No. 2.8e-35;
Matches 138; Conservative 34; Mismatches 65; Indels 17; Gaps 5;

QY 3 QVQLQSGAELARPGASVKMSCKASGYTFTTTHHWVRQPGHDLHWIGYINPSSGYSDY 62
DB 1 QVQLVQSGAEVKPKGASVKSCASGYTFTSYISWVRQAPGQGLEWMGMNPNSTGY 60
QY 63 NQPFKGTTLTADKSNATYMWLNLSLTSDSAVYYCARRADYGNY-----EYTFAYWGQ 117
DB 61 AQKFGQRTVMTSDTSSTAYMELSLRSDDTAVYCAR---GQYDILTGYNWFDPWGR 116
QY 118 GTTVTVSS---AKTTPKLGDIQAVVTQESALTTSPGETVTLTCRSNTGTVTTSNYANWV 174
DB 117 GLTVTVSSGGSGGGSGGGSSSELQDPAVSVALGQTVRITCQ---GDSLRSYYASWY 173
QY 175 QKPDHLFTGLHTNNRPAQVPARFSGSLIGDKAALTITGAQTEDEAIYFCAL--WYNN 232
DB 174 QKPGQAPVLVIYGNKNRPSGVPDRFSGSSSGNTASLTITGAQAEDEADYYCNXRDS 233
QY 233 HVVFGGQTKLTVLG 246
DB 234 HVVFGGQTKLTVLG 247

RESULT 9
US-11-054-515-1643
; Sequence 1643, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
```

; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1643  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1643

Query Match 44.3%; Score 651; DB 7; Length 248;  
Best Local Similarity 53.9%; Pred. No. 3.1e-35;  
Matches 136; Conservative 35; Mismatches 63; Indels 20; Gaps 6;

QY 3 QVQLQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLHWIGYINPSSGYSYD 62  
DB 1 QVQLQSGAEVKPGASVKVSKASGYTFYTHHWVRQAPGQGLEWMGINSGGDTKY 60  
QY 63 QNPFKGTTLTADKSNNTAYMQLNSLTSEDSAVYICARRADYG---NYEYTWFAWCOGT 119  
DB 61 SRKFGQGVITTKDTSASAYMELSLGSEDTALYCA-RATYDPLTGYSGDFDIWQGT 119  
QY 120 TTVTVSS---AKTTPKLGDIQAVVTOESALTSPEGTTLTCSRNTGTVTTSYANWVQE 176  
DB 120 LVTVSSGGGGGGGGGGSSSELQDPVAVSVALGQTVITCO---GDSLSRYASYWYQ 176  
QY 177 KPDLHLFTGLIGHTNNRPGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYN----- 231  
DB 177 KPGQAPVLVIYGNKRRSGIPDRFSGSSSGNTASLTITGAQAEADYYC-----NSRDS 232  
QY 232 -NHVFGGKTKLVLG 246  
DB 233 GNVVFGGKTKLVLG 248

RESULT 10  
US-11-054-515-1723  
; Sequence 1723, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1643  
; LENGTH: 248

; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1723  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1723

Query Match 44.3%; Score 651; DB 7; Length 250;  
Best Local Similarity 52.9%; Pred. No. 3.1e-35;  
Matches 136; Conservative 36; Mismatches 65; Indels 20; Gaps 5;

QY 3 QVQLQSGAELARPGASVKMSCKASGYTFYTHHWVRQPGHDLHWIGYINPSSGYSYD 62  
DB 1 EVQLQSGAEVKPGASVKVSKASGYTFYTHHWVRQAPGQGLEWMGINPNSGGTNY 60  
QY 63 QNPFKGTTLTADKSNNTAYMQLNSLTSEDSAVYICARRADY---GNVEYTWFAWCOG 118  
DB 61 AQKFGQGVITMTDTSISATYMLSLRSDDTAVYICARVLPHYDILTGYSONWFDPMKG 120  
QY 119 TTVTVSS---AKTTPKLGDIQAVVTOESALTSPEGTTLTCSRNTGTVTTSYANWVQ 175  
DB 121 TMTVSSGGGGGGGGGGSSSELQDPVAVSVALGQTVITCO---GDSLSRYASYWYQ 177  
QY 176 EKPDHLFTGLIGHTNNRPGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYN----- 231  
DB 178 QKPGQAPVLVIYGNKRRSGIPDRFSGSSSGNTASLTITGAQAEADYYC-----NSRDS 233  
QY 232 -NHVFGGKTKLVLG 246  
DB 234 GNVVFGGKTKLVLG 250

RESULT 11  
US-11-054-515-927  
; Sequence 927, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 927  
; LENGTH: 247

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-927

Query Match      44.3%; Score 650.5; DB 7; Length 247;
Best Local Similarity 53.9%; Pred. No. 3.3e-35;
Matches 137; Conservative 35; Mismatches 65; Indels 17; Gaps 5;

QY 3 QVQLQSGAELARPASVSKASGYTFTTTHHWVRQPGHDLRWIGYINPSSGYSY 62
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFTTTHHWVRQPGHDLRWIGYINPSSGYSY 60
QY 63 NONFKGKTTLTADKSNATYMQLSLTSDSAVYYCAR-----EYTWFAWQ 117
Db 61 AOKFQGRVITADKSNATYMQLSLTSDSAVYYCAR-----EYTWFAWQ 116
QY 63 NONFKGKTTLTADKSNATYMQLSLTSDSAVYYCARADYCN-----EYTWFAWQ 117
Db 61 AOKFQGRVITADKSNATYMQLSLTSDSAVYYCAR-----EYTWFAWQ 116
QY 118 GTTIVTVSS---AKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSNYANW 174
Db 117 GTLTVTVSSGGGGGGGGGGSSSELTQDPVSVVALGQTVRITCQ---GDSLSRYASWY 173
QY 175 QKPKOHLFTGLIGHTNNRPAQVPARFSGSLIGDKAALTTTGAQTEDEAIYFCALM--YNN 232
Db 174 QKPKQAPVLVIYKGNRPSPGIDPRFSGSSGNTASLTITGAQAEDEADYYCNSQDSGN 233
QY 233 HWVFGGKTLTVLG 246
Db 234 HWVFGGKTLTVLG 247

RESULT 12
US-11-054-515-893
; Sequence 893, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 893
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-893

Query Match      44.1%; Score 649; DB 7; Length 248;
Best Local Similarity 53.7%; Pred. No. 4.1e-35;
Matches 139; Conservative 35; Mismatches 59; Indels 26; Gaps 6;

QY 3 QVQLQSGAELARPASVSKASGYTFTTTHHWVRQPGHDLRWIGYINPSSGYSY 62
Db 1 QVQLVQSGAEVKKPGASVKSCASGYTFTTTHHWVRQPGHDLRWIGYINPSSGYSY 60
QY 63 NONFKGKTTLTADKSNATYMQLSLTSDSAVYYCARRADYCN-----EYTWFAWQ 119
Db 61 SRKFGGRVITADKSNATYMQLSLTSDSAVYYCARRADYCN-----EYTWFAWQ 119
QY 120 TWTVSS---AKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSNYANW 176
Db 120 LVTVSSGGGGGGGGGGSSSELTQDPVSVVALGQTVRITCQ---GDSLSRYASWY 176

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1681

Query Match      44.0%; Score 647; DB 7; Length 248;
Best Local Similarity 53.5%; Pred. No. 5.5e-35;
Matches 137; Conservative 36; Mismatches 63; Indels 20; Gaps 6;

QY 3 QVQLQSGAELARPASVSKASGYTFTTTHHWVRQPGHDLRWIGYINPSSGYSY 62
Db 1 QVQLQSGAELARPASVSKASGYTFTTTHHWVRQPGHDLRWIGYINPSSGYSY 60
QY 63 NONFKGKTTLTADKSNATYMQLSLTSDSAVYYCARRADYCN-----EYTWFAWQ 119
Db 61 SRKFGGRVITADKSNATYMQLSLTSDSAVYYCARRADYCN-----EYTWFAWQ 119
QY 120 TWTVSS---AKTTPKLGDDIQAVVTOESALTTSPGETVTLTCSRNTGTVTTSNYANW 176
Db 120 LVTVSSGGGGGGGGGGSSSELTQDPVSVVALGQTVRITCQ---GDSLSRYASWY 176
```

Qy 177 KPDHLFTGLTHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYN----- 231  
Db 177 KPGQAPVLVIYGNRRPSGIPDRFSGSSSGNTASLITGAQAEADAYYC-----NSRDSS 232  
Qy 232 -NHWFVGGGKTLTVLG 246  
Db 233 GNHVFVGGGKTLTVLG 248

RESULT 14  
US-11-054-515-1496  
; Sequence 1496, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1496  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1496

Query Match 44.0%; Score 646.5; DB 7; Length 251;  
Best Local Similarity 52.8%; Pred. No. 6e-35;  
Matches 133; Conservative 40; Mismatches 70; Indels 9; Gaps 5;  
Qy 3 QVQLQSGAEIARPGASVYKMSCKASGYTFYTHHWVRQRPQGHDLWIGYINPSSGYSYD 62  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYSTYSYTHHWVRQAPGQRLRWGMINVGNTKY 60  
Qy 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVVYCARADYGYE-YTWFA-YWGQGT 120  
Db 61 SQKLQGRVITTRDISASTAYMELSSRLSEDTAVYICA-RSDYDILTGYIWPVAVWGQGT 119  
Qy 121 VTVS-----SAKTTPKLGGDIQAVVTQESALTTSPGETVTLTCSRNTGTVTTSYANWVQ 175  
Db 120 VTVSSGGGGGGGGGGGSAQSGLVLTQPPSAGSPGQSVTISCTGGSSDVGGYNYVMYQ 179  
Qy 176 EKPDLHFTGLTHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWY--NNHW 234  
Db 180 QYPGKAPKLIYNEVKKRPSGVPDRFSGSKSGNTASLTVSGLQAEDEANYCASYAGNNV 239  
Qy 235 VFGGKTLTVLG 246  
Db 240 VFGGKTLTVLG 251

RESULT 15

US-11-054-515-2082  
; Sequence 2082, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2082  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-2082

Query Match 43.9%; Score 646; DB 7; Length 254;  
Best Local Similarity 51.6%; Pred. No. 6.5e-35;  
Matches 131; Conservative 35; Mismatches 78; Indels 10; Gaps 3;  
Qy 3 QVQLQSGAEIARPGASVYKMSCKASGYTFYTHHWVRQRPQGHDLWIGYINPSSGYSYD 62  
Db 1 QVQLVQSGADVKKPGASVYKMSCKASGYTTSYTHHWVRQAPGRLRWGMINPSSGATNY 60  
Qy 63 NQPFKGTTLTADKSSNTAYMQLNSLTSEDSAVVYCARADYGYE---YTWFA-YWGQGT 119  
Db 61 AQFQGRVITTRDTSSSTVYMEUSSLRFEDTAIYICVRDADEGLVFAETTNWFDWGQGT 120  
Qy 120 TVTVS-----SAKTTPKLGGDIQAVVTQESALTTSPGETVTLTCSRNTGTVTTSYANWV 174  
Db 121 MVTVSSGGGGGGGGGGGSAQSGLVLTQPPSVSGAPQSVTISCTGGSSNIGASVDVNWY 180  
Qy 175 QEPKDLHFTGLTHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIYFCALWYN--N 232  
Db 181 QQLPGTAPKLLISGNTNRPSGVPDRFSGNSGTSASLAITGLQAEDEADYVCQSYDNL 240  
Qy 233 HWYFGGKTLTVLG 246  
Db 241 GWVFGGKTLTVLG 254

Search completed: February 9, 2006, 04:00:32  
Job time : 20.9009 secs

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